

Figure 1A

1 CACCCTATCC TACACTACTA GGAAGTTCGA CAGTCCGCCT CGGGCAGCCC AAAGCTCCTC 60
 61 TGCCACACCT GGCTCCCAAA ACCCTCCAAA ACAAAAGACC AGAAAAGCAC TCTCCACCCA 120
 121 GCAGCCAAAC GCCTCCTTCT TGACGCCAGC CCCACCCCTC TGTCTGCTCG AGCCAGGAA 180
 181 AGGCCTGAAG GAACAGGCCG GGAAGGAGC CCTCCCTCTC TCCCTTGTC CTTCCATCCAC 240
 241 CCAGCGCCCG CATCTGGAGA CCCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300
 1 M A R A H W G C C P W L 12
 301 GTCTCCTCTT GTGCTTGTGC CTGGGGCCAC ACAAGCCAC TGGACCTTGG AGGCAGGAT 360
 13 V L L C A C A W G H T K P L D L G G Q D 32
 361 GTGAGAAATT GTTCCACCAA CCCCCCTTAC CTTCAGTTA CTGTGGTCAA TACCACAATG 420
 33 V R N C S T N P P Y L P V T V V N T T M 52
 421 TCACTCACAG CCCTCCGCCA GCAGATGCAG ACCCAGAATC TCTCAGCCTA CATCATCCCA 480
 53 S L T A L R Q Q M Q T Q N L S A Y I I P 72
 481 GGCACAGATG CTCACATGAA CGAGTACATC GGCCAACATG ACGAGAGGCG TGCCTGGATT 540
 73 G T D A H M N E Y I G Q H D E R R A W I 92
 541 ACAGGCTTTA CAGGCTCTGC AGGAAGTCCA GTGGTGACTA TGAAGAAAGC AGCTGTCTGG 600
 93 T G F T G S A G T A V V T M K K A A V W 112
 601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAAAATG ACTGTAATTG GGAGCTCCAT 660
 113 T D S R Y W T Q A E R Q M D C N W E L H 132
 661 AAGGAAGTTG GCACCACTCC TATTGTCAAC TGGCTCCTCA CCGAGATTCC CGCTGGAGGG 720
 133 K E V G T T P I V T W L L T E I P A G G 152
 721 CGTGTGGGTT TTGACCCCTT CCTCTTGTC ATTGACACT GGGAGAGTTA TGATCTGGCC 780
 153 R V G F D P F L L S I D T W E S Y D L A 172
 781 CTCCAAGGCT CTAACAGACA GCTGGTGTCC ATCACAACCA ATCTTGTGGA CCTTGTATGG 840
 173 L Q G S N R Q L V S I T T N L V D L V W 192
 841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTATTG CCCTGCAGGA GGCATTACA 900
 193 G S E R P P V P N Q P I Y A L Q E A F T 212
 901 GGGAGCACTT GGCAGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAAG 960
 213 G S T W Q E K V S G V R S Q M Q K H Q K 232

Figure 1B

961 GTCCCGACTG CGTCCTTCT GTCGGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020
 233 V P T A V L L S A L E E T A W L F N L R 252

1021 GCCAGTGAAC TCCCTATAA CCCCTTCTC TATTCCTACA CGCTGCTCAC AGACTCTTCT 1080
 253 A S D I P Y N P F F Y S Y T L L T D S S 272

1081 ATTAGTGTG TTGCAACAA GAGTCGCTT AGCTCCGAAA CCTTGAGCTA TCTGAACCTC 1140
 273 I R L F A N K S R F S S E T L S Y L N S 292

1141 AGTTGCACAG GCCCATGTG TGTGCAATC GAGGATTACA GCCAAGTTCG TGACAGCATC 1200
 293 S C T G P M C V Q I E D Y S Q V R D S I 312

1201 CAGGCTTACT CATTTGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260
 313 Q A Y S L G D V R I W I G T S Y T M Y G 332

1261 ATCTATGAAA TGATACCAAG GGAGAAACTC GTGACAGACA CCTACTCCCC AGTGATGATG 1320
 333 I Y E M I P R E K L V T D T Y S P V M M 352

1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGGGGGAC 1380
 353 T K A V K N S K E Q A L L K A S H V R D 372

1381 GCTGTGGCTG TGATCCGTA CTTGGTCTGG CTGGAGAAGA ACGTGCCCAA AGGCACAGTG 1440
 373 A V A V I R Y L V W L E K N V P K G T V 392

1441 GATGAGTTTT CGGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAACA GTTCTCCTCC 1500
 393 D E F S G A E I V D K F R G E E Q F S S 412

1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTTGAATG CTGCCCTGGC CCACTACAGC 1560
 413 G P S F E T I S A S G L N A A L A H Y S 432

1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620
 433 P T K E L N R K L S S D E M Y L L D S G 452

1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCCTCT 1680
 453 G Q Y W D G T T D I T R T V H W G T P S 472

1681 GCCTTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740
 473 A F Q K E A Y T R V L I G N I D L S R L 492

1741 ATCTTTCCCG CTGCTACATC AGGGCGAATG GTGGAGGCCT TTGCCCGCAG AGCCTTGTGG 1800
 493 I F P A A T S G R M V E A F A R R A L W 512

1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGGCA TTGGCAACTT CCTGTGTGTG 1860
 513 D A G L N Y G H G T G H G I G N F L C V 532

Figure 1C

1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920
 533 H E W P V G F Q S N N I A M A K G M F T 552

1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTGTGGA TCCGTCTCGA AGATGTGGCT 1980
 553 S I E P G Y Y K D G E F G I R L E D V A 572

1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATTT 2040
 573 L V V E A K T K Y P G E L P D L V V S F 592

2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCCCAGCA TCTCCAGTAC 2100
 593 V P Y D R N L I D V S L L S P E H L Q Y 612

2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGGTC CAGAGCTGCA GAGGCGCCAG 2160
 613 L N R Y Y Q T I R E K V G P E L Q R R Q 632

2161 CTACTAGAGG AGTTCGAGTG GCTTCAACAG CACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220
 633 L L E E F E W L Q Q H T E P L A A R A P 652

2221 GACACCGCCT CCTGGGCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGTGAGAGT 2280
 653 D T A S W A S V L V V S T L A I L G W S 672

2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACC CTCCATCTAG ATGGGGGGCT CCTTGCTTAA 2340
 673 V * 673

2341 GCTCCCTCA CCCTGCACGT AACATACCCC AAGAGCCCTT GCTGGCCCAT TGCCTAGAAA 2400

2401 CCTTTGCAAT CATCCTCCTT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460

2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCGC GGGTTGTATA CCACACCTTG 2520

2521 GGCCCCAAT CCCAGGCCCC GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580

2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCTCT CCGCCAACA 2640

2641 AAGCCCCAAG AAAACAATGC CCCTAOCACC CAAGGGTGCC ATGGTCCCGG GAAACCCCAA 2700

2701 CCTGTCAACG CGTGTGTGGC GTAACCAGAA CTGTTCCCCC CCACCAAGGC TTAATAATCG 2760

2761 CCCCCCATTT TTAACCATCG TCCATTAAAC ACCTGTGTGG CATAGCCAGA GCTGTTCGAA 2820

2821 CCCAGCCAGG GATGAAAAAT CAACCCCGCA CATGGAACCC ATGATTCCTA AACCCGGGGT 2880

2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTTGGC TGTGGAGTAA 2940

Figure 1D

2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCCTACCA GAGGTGGAG AACAAACTTG 3000
 3001 GGCAGCCGGA ACCCGTCACT ATTTTAGATT CTTGGCATTG GAGGAGCCCT TTGAACTTTC 3060
 3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCA CATTTCTTGG ATGCCCTTTC 3120
 3121 ACCTTGTGTG GACAGTGTCT GGTTCGCCA TTTTACAGAC AGGAAAAC TG AGCTTCAGAC 3180
 3181 AGGGGTTGGG CTTTGCCTAA GGACACACAA ATTTGTTGG GAGTTGATGG GGCCAGATGA 3240
 3241 GCCAGCATTC CAGCTGTTTC ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCA 3300
 3301 GCCCTCTCCT CATTCCTGA ACCCACTGTG GTGAGAAGAA TTGCTCCGG CCAAATTGGC 3360
 3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTTAA ACAGCCTAAC AAAGACACTT 3420
 3421 GCCTGTGG 3428

Figure 2A

1 CACCCCTATCC TACACTACTA GGAACCTGCA CAGTCCGCT CGGGCAGCCC AAAGCTCCTC 60
 61 TGCCCCACCT GGCTCCCAA ACCTCCCAA ACAAAAGACC AGAAAAGCAC TCTCCACCA 120
 121 GCAGCCAAAC GCCTCCTTCT TGACGCCAGC CCCCACCTC TGTCTGCTCG AGCCACAGAA 180
 181 AGGCCTGAAG GAACAGGCCG GGAAGGAGC CCTCCCTCTC TCCCTTGTC CTCCATCCAC 240
 241 CCAGCGCCGG CATCTGGAGA CCCTATGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300
 1 M A R A H W G C C P W L 12
 301 GTCTTCCTCT GTGCTGTGTC CTGGGCCAC ACAAAAGCCAC TGGACCTGG AGGCAGGAT 360
 13 V L L C A C A W G H T K P L D L G G Q D 32
 361 GTGAGAAAT GTTCCACCAA CCCCCCTTAC CTTCAGTTA CTGTGGTCAA TACCACAATG 420
 33 V R N C S T N P P Y L P V T V V N T T M 52
 421 TCACTCAGC CCCTCCGCCA GCAGATGCAG ACCCAGAATC TCTCAGCCTA CATCATCCCA 480
 53 S L T A L R Q Q M Q T Q N L S A Y I I P 72
 481 GGCACAGATG CTCACATGAA CGAGTACATC GGCCAACATG ACGAGAGGCG TGCCTGGATT 540
 73 G T D A H M N E Y I G Q H D E R R A W I 92
 541 ACAGGCTTTA CAGGGTCTGC AGGAACTGCA GTGGTGACTA TGAAGAAAGC AGCTGTCTGG 600
 93 T G F T G S A G T A V V T M K K A A V W 112
 601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAAATGG ACTGTAATTG GGAGCTCCAT 660
 113 T D S R Y W T Q A E R Q M D C N W E L H 132
 661 AAGGAAGTTG GCACCACTCC TATGTGTCACC TGGCTCCTCA CGAGATTCC CGCTGGAGGG 720
 133 K E V G T T P I V T W L L T E I P A G G 152
 721 CGTGTGGGTT TTGACCCCTT CCTCTTGTC ATTGACACT GGGAGAGTTA TGATCTGGCC 780
 153 R V G F D P F L L S I D T W E S Y D L A 172
 781 CTCCAAGGCT CTAACAGACA GCTGGTGTC ATCACAACCA ATCTTGTTGA CCTGGTATGG 840
 173 L Q G S N R Q L V S I T T N L V D L V W 192
 841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTATG CCCTGCAGGA GCATTCACA 900
 193 G S E R P P V P N Q P I Y A L Q E A F T 212
 901 GGGAGCACTT GGCAGGAGAA AGTATCTGCG GTCCGAAGCC AGATGCAGAA GCATCAAAAG 960
 213 G S T W Q E K V S G V R S Q M Q K H Q K 232

Figure 2B

961 GTCCCGACTG CCGTCCTTCT GTCGGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020
 233 V P T A V L L S A L E E T A W L F N L R 252

1021 GCCAGTGACA TCCCTATATA CCCCTTCTTC TATTCTTACA CGCTGCTCAC AGACTCTTCT 1080
 253 A S D I P Y N P F F Y S Y T L L T D S S 272

1081 ATTAGOTTTG TTGCAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAAGTCC 1140
 273 I R L F A N K S R F S S E T L S Y L N S 292

1141 AGTTGCACAG GCCCATGTG TGTGCAATC GAGGATTACA GCCAAGTTCG TGACAGCATC 1200
 293 S C T G P M C V Q I E D Y S Q V R D S I 312

1201 CAGGCCTACT CATTGGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATTGG 1260
 313 Q A Y S L G D V R I W I G T S Y T M Y G 332

1261 ATCTATGAAA TGATACCAAG GGAGAAACTC GTGACAGACA CCTACTCCCC AGTGATGATG 1320
 333 I Y E M I P R E K L V T D T Y S P V M M 352

1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA COTGCGGGAC 1380
 353 T K A V K N S K E Q A L L K A S H V R D 372

1381 GCTGTGGCTG TGATCCGGTA CTTGGTCTGG CTGGAGAAGA ACGTGCCCAA AGGCACAGTG 1440
 373 A V A V I R Y L V W L E K N V P K G T V 392

1441 GATGAGTTTT CGGGGGCAGA GATCGTGGAC AAGTCCGAG GAGAAGAACA GTTCTCCTCC 1500
 393 D E F S G A E I V D K F R G E E Q F S S 412

1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTTGAATG CTGCCCTGGC CCACTACAGC 1560
 413 G P S F E T I S A S G L N A A L A H Y S 432

1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620
 433 P T K E L N R K L S S D E M Y L L D S S G 452

1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCTCTT 1680
 453 G Q Y W D G T T D I T R T V H W G T P S 472

1681 GCCTTTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740
 473 A F Q K E A Y T R V L I G N I D L S R L 492

1741 ATCTTTCCCG CTGCTACATC AGGCGAATG GTGGAGGCGT TTGCCCGCAG AGCCTTGTGG 1800
 493 I F P A A T S G R M V E A F A R R A L W 512

1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGCAG TTGGCAACTT CTTGTGTGTG 1860
 513 D A G L N Y G H G T G H G I G N F L C V 532

Figure 2C

1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920
 533 H E W P V G F Q S N N I A M A K G M F T 552

1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTGTGGG TCCGTCTCGA AGATGTGGCT 1980
 553 S I E P G Y Y K D G E F G I R L E D V A 572

1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATTT 2040
 573 L V V E A K T K Y P G E L P D L V V S F 592

2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCCGAGCA TCTCCAGTAC 2100
 593 V P Y D R N L I D V S L L S P E H L Q Y 612

2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGGTC CAGAGCTGCA GAGGCGCCAG 2160
 613 L N R Y Y Q T I R E K V G P E L Q R R Q 632

2161 CTACTAGAGG AGTTCGAGTG GCTTCAACAG CACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220
 633 L L E E F E W L Q Q H T E P L A A R A P 652

2221 GACACCCGCT CCITGGCCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGCTGGAGT 2280
 653 D T A S W A S V L V V S T L A I L G W S 672

2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACC CTCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340
 673 V * 673

2341 GCTCCCCCTA CCCTGCACTG AACATACCCC AAGAGCCCTT GCTGGCCCAT TGCCTAGAAA 2400

2401 CCTTTGCATT CATCCTCCTT CTCCAAGACC TATGGAGAAG GTCCAGGCC CCAGGAACAA 2460

2461 CAGGGCTTCT TGSCCCGAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCCCTG 2520

2521 GGCCCCTAAT CCCAGGCCCC GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580

2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCCCT CGGCCAAACA 2640

2641 AAGCCCCAAG AAAACAATGC CCCTACCACC CAAGGGTGCC ATGGTCCCCG GAAAACCCAA 2700

2701 CCTGTCAACG CGTGTGTGGC GTAACCAGAA CTGTTCCCCC CCACGAGGC TTAARAATCG 2760

2761 CCCCCCATTT TTAACCATCG TCCATTAAAC ACCTGGTGGG CATAGCCAGA GCTGTTCGAA 2820

2821 CCCAGCCAGG GATGAAAAAT CAACCCCGGA CATGGAACCC ATGATTCTTA AACCCGGGT 2880

2881 AGGTTCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTTGGC TGTGGAGTAA 2940

Figure 2D

2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCATCCA GAGGTTGGAG AACAAACTTG 3000

3001 GGCAGCCGGA ACCCGTCACT ATTTTAGATT CCTGGCATTG GAGGAGCCCT TTGAACCTTC 3060

3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCA CATTTCTGG ATGCCCTTC 3120

3121 ACCTTGTGTG GACAGTGTCT GGTTCCTCCA TTTTACAGAC AGGAAAAGTG AGCTTCAGAC 3180

3181 AGGGGGTGGG CTTTGCTTAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240

3241 GCCAGCATTC CAGCTGTTTC ACCCTTCAGC AACATGCAGA GTCCTTGAGC CCACCTCCCA 3300

3301 GCCCTCTCCT CATTCCTGTA ACCCACTGTG GTGAGAGAA TTTGCTCCGG CCAAATTGGC 3360

3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTTAAA ACAGCCTAAC AAAGACACTT 3420

3421 GCCTGTGG 3428

Figure 3A

1 CTGTGCATGG CATCATCCTG GCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGTCT 60
 1 M A S S W P P L E L Q S S N Q S Q L 18

 61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19 F P Q N A T A C D N A P E A W D L L H R 38

 121 GTGTGCGGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTCT 180
 39 V L P T F I I S I C F F G L L G N L F V 58

 181 CTGTGTGGTCT TCCTCTGGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59 L L V F L L P R R Q L N V A E I Y L A N 78

 241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GCTTGGCCCT TCTGGGCAGA GAATATCTGG 300
 79 L A A S D L V F V L G L P F W A E N I W 98

 301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTATCATAG 360
 99 N Q F N W P F G A L L C R V I N G V I K 118

 361 GCCAATTGTG TCATCAGCAT CTTCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
 119 A N L F I S I F L V V A I S Q D R Y R V 138

 421 CTGTGTCAACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTCACTGTC 480
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

 481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCTGTCT GCGATCCATC 540
 159 V L I W V V G G L L S I P T F L L R S I 178

 541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCACTCTGC TCCTCCCCCA TGAGGCCTGG 600
 179 Q A V P D L N I T A C I L L L P H E A W 198

 601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
 199 H F A R I V E L N I L G F L L P L A A I 218

 661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
 219 V F F N Y H I L A S L R T R E E V 238

 721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCAGCCT CGTGGTTGCC 780
 239 R V R G P K D S K T T A L I T A L V V A 258

 781 TTCTGTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCCTTC TGGAAATCTT ATTCCAGGTG 840
 259 F L V C W A P Y H F F A F L E F L F Q V 278

 841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCTGCA ATTGGCCAAC 900
 279 Q A V R G C F W E D F I D L G L Q L A N 298

Figure 3B

901	TTCCTTGGCT	TCACTAACAG	CTCCCTGAAT	CCAGTAATTT	ATGTCCTTGT	GGGCCGGGTC	960
299	F F A F	T N S	S L N	P V I Y	V F V	G R L	318
961	TTCAGGACCA	AGGTCTGGGA	ACTTTATAAA	CAATGCACCC	CTAAAGTCT	TGCTCCAATA	1020
319	F R T K	V W E	L Y K	Q C T P	K S L	A P I	338
1021	TCTTCATCCC	ATAGGAAAGA	AATCTTCCAA	CTTTTCTGGC	GGAATTAATA	CAGCATTGAA	1080
339	S S S H	R K E	I F Q	L F W R	N *		353

1081 CC 1082

Figure 4A

1 CTGTGTCATGG CATCATCCTG GCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
 1 M A S S W P P L E L Q S S N Q S Q L 18

 61 TTCCCTCAAA ATGCTACGGC CTGTGACAAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19 F P Q N A T A C D N A P E A W D L L H R 38

 121 GTGTGCGCGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGA CCTTTTGTCT 180
 39 V L P T F I I S I C F F G L L G N L F V 58

 181 CTGTTGGTCT TCCTCTGCC CGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59 L L V F L L P R R Q L N V A E I Y L A N 78

 241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGGCCT TCTGGGCAGA GAATATCTGG 300
 79 L A A S D L V F V L G L P P W A E N I W 98

 301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTATCAAG 360
 99 N Q F N W P F G A L L C R V I N G V I K 118

 361 GCCAATTGTG TCATCAGCAT CTCTCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
 119 A N L F I S I F L V V A I S Q D R Y R V 138

 421 CTGTGTCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAAGCCCG GGTACCTGC 480
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

 481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
 159 V L I W V V G G L L S I P T F L L R S I 178

 541 CAAGCCGTCC CAGATCTGAA CATCACCACC TGCATCTGCT TCCTCCCCCA TGAGGCGCTG 600
 179 Q A V P D L N I T A C I L L L P H E A W 198

 601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGTGCGGATC 660
 199 H F A R I V E L N I L G F L L P L A A I 218

 661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
 219 V F N Y H I L A S L R T R E E V S R T 238

 721 AGAGTGCGGG GGCGGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCAGCT CGTGTTGCTC 780
 239 R V R G P K D S K T T A L I L T L V V A 258

 781 TTCTCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGAATTCTT ATTCCAGGTG 840
 259 F L V C W A P Y H F F A F L E F L F Q V 278

 841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGAAC TGGGCTTGCA ATTGCCAAC 900
 279 Q A V R G C F W E D F I D L G L Q L A N 298

Figure 4B

901 TTCTTTGCGT TCACTAACAG CTCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCAGCTC 960
299 F F A F T N S S L N P V I Y V F V G Q L 318

961 TTCAGGACCA AGGTCCTGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

1081 CC 1082

Figure 5A

1 CTGTGCAATGG CATCATCCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
 1 M A S S W P P L E L Q S S N Q S Q L 18
 61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19 F P Q N A T A C D N A P E A W D L L H R 38
 121 GTGTGCGCAA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTTC 180
 39 V L P T F I I S I C F F G L L G N L F V 58
 181 CTGTGTGGTCT TCCTCCTGCC CGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59 L L V F L L P R R Q L N V A E I Y L A N 78
 241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
 79 L A A S D L V F V L G L P F W A E N I W 98
 301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCGCTG TCATCAACGG GGTTCATCAAG 360
 99 N Q F N W P F G A L L C R V I N G V I K 118
 361 GCCAAATTGT TCATCAGCAT CTTCCTGGTG GTGCCATCA GCCAGGACCG CTACCGCGTG 420
 119 A N L F I S I F L V V A I S Q D R Y R V 138
 421 CTGTGTCAACC CTAATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTCACTGTC 480
 139 L V H P M A S G R Q Q R R R Q A R V T C 158
 481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
 159 V L I W V V G G L L S I P T F L L R S I 178
 541 CAAGCGCTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
 179 Q A V P D L N I T A C I L L L P H E A W 198
 601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGTGCGGATC 660
 199 H F A R I V E L N I L G F L L P A A I 218
 661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAAGCG GGGAGGAGT CAGCAGGACA 720
 219 V F N W Y H I L A S L R T R E E V C A G 238
 721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCAGCTG CGTGGTTGTC 780
 239 R V R G P K D S K T T A L L T L V V A 258
 781 TTCTCTGGTCT GCTGGGCCCC TTACCACTTC TTTCCTTCC TGAATTCTTT ATTCCAGGTG 840
 259 F L V C W A P Y H F F A F L E F L F Q V 278
 841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCTTGCA ATTGGCCAAC 900
 279 Q A V R G C F W E D F I D L G L Q L A N 298

Figure 5B

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901 TTCTTTGCCT TCACTAACAG CTCCTTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGCTCTGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

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Figure 6A

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1  ATGTTCTCTC  CCTGGAAGAT  ATCAATGTTT  CTGTCTGTTC  GTGAGGACTC  CGTGCCCACT  60
1  M  F  S  P   W  K  I   S  M  F   L  S  V  R   E  D  S   V  P  T   20

61  ACGGCCTCTT  TCAGCGCCGA  CATGCTCAAT  GTCACCTTGC  AAGGGCCCAAC  TCTTAACGGG  120
21  T  A  S  F   S  A  D   M  L  N   V  T  L  Q   G  P  T   L  N  G   40

121  ACCTTTGCCC  AGAGCAAATG  CCCCCAAGTG  GAGTGGCTGG  GCTGGCTCAA  CACCATCCAG  180
41  T  F  A  Q   S  K  C   P  Q  V   E  W  L  G   W  L  N   T  I  Q   60

181  CCCCCCTTCC  TCTGGGTGCT  GTTCGTGCTG  GCCACCCTAG  AGAACATCTT  TGTCCCTCAGC  240
61  P  P  F  L   W  V  L   F  V  L   A  T  L  E   N  I  F   V  L  S   80

241  GTCTTCTGCC  TGCACAAGAG  CAGCTGCACG  GTGGCAGAGA  TCTACCTGGG  GAACCTGGCC  300
81  V  F  C  L   H  K  S   S  C  T   V  A  E  I   Y  L  G   N  L  A   100

301  GCAGCAGACC  TGATCTGGC  CTGCGGGCTG  CCCTTCTGGG  CCATCACCAT  CTCCAACAAC  360
101  A  A  D  L   I  L  A   C  G  L   P  F  W  A   I  T  I   S  N  N   120

361  TTCGACTGGC  TCTTTGGGGA  GACGCTCTGC  CGCGTGGTGA  ATGCCATTAT  CTCCATGAAC  420
121  F  D  W  L   F  G  E   T  L  C   R  V  V  N   A  I  I   S  M  N   140

421  CTGTACAGCA  GCATCTGTTT  CCTGATGCTG  GTGAGCATCG  ACCGCTACCT  GGCCCTGGTG  480
141  L  Y  S  S   I  C  F   L  M  L   V  S  I  D   R  Y  L   A  L  V   160

481  AAAACCATGT  CCATGGGCGG  GATGCGCGGG  GTGCGCTGGG  CCAAGCTCTA  CAGCTTGGTG  540
161  K  T  M  S   M  G  R   M  R  G   V  R  W  A   K  L  Y   S  L  V   180

541  ATCTGGGGGT  GTACGCTGCT  CCTGAGCTCA  CCCATGCTGG  TGTTCGGGAC  CATGAAGGAG  600
181  I  W  G  C   T  L  L   L  S  S   P  M  L  V   F  R  T   M  K  E   200

601  TACAGCGATG  AGGGCCACAA  CGTCACCGCT  TGTGTCATCA  GCTACCCATC  CCTCATCTGG  660
201  Y  S  D  E   G  H  N   V  T  A   C  V  I  S   Y  P  S   L  I  W   220

661  GAAGTGTTCA  CCAACATGCT  CCTGAATGTC  GTGGGCTTCC  TGCTGCCCTT  GAGTGTCACT  720
221  E  V  F  T   N  M  L   L  N  V   V  G  L  V   L  P  L   L  F  I   240

721  ACCTTCTGCA  CGATGCAGAT  CATGCAGGTG  CTGCGGAACA  ACGAGATGCA  GAAGTTCAAG  780
241  T  F  N  C   M  Q  I   M  Q  V   L  R  N  N   E  M  Q   K  F  T   260

781  GAGATCCAGA  CGGAGAGGAG  GGCCACGGTG  CTAGTCTCTG  TTGTGCTGCT  GCTATTTCATC  840
261  E  I  Q  T   E  R  R   A  T  V   L  V  L  V   V  L  L   L  F  I   280

841  ATCTGTCTGC  TGCCCTTCCA  GATCAGCACC  TTCTTGGATA  CGCTGCATCG  CCTCGGCATC  900
281  I  C  W  L   P  F  Q   I  S  T   F  L  D  T   L  H  R   L  G  I   300

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Figure 6B

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901 CTCTCCAGCT . GCCAGGACGA . GGCATCATC . GATGTAATCA . CACAGATCGC . CTCCTTCATG . 960
301 L S S C . Q D E . R I I . D V I T . Q I A . S F M . 320

961 GCCTACAGCA . ACAGCTGCCT . CAACCCACTG . GTGTACGTGA . TCCTGGGCAA . GCGCTTCCGA . 1020
321 A Y S N . S C L . N P L . V Y V I . V G K . R F R . 340

1021 AAGAAGTCTT . GGGAGGTGTA . CCAGGGAGTG . TGCCAGAAAG . GGGGCTGCAG . GTCAGAACCC . 1080
341 K K S W . E V Y . Q G V . C Q K G . G C R . S E P . 360

1081 ATTCTAGATGG . AGAATCCAT . GGGCACACTG . CGGACCTCCA . TCTCCGTGGA . ACGCCAGATT . 1140
361 I Q M E . N S M . G T L . R T S I . S V E . R Q I . 380

1141 CACAAATGCG . AGGACTGGGC . AGGGAGCAGA . CAGTGAGCAA . ACGCCAGCAG . GGCTGCTGTG . 1200
381 H K L Q . D W A . G S R . Q * . 391

1201 AATTGTGTGA . AGGATTGAGG . GACAGTTGCT . TTTCAGCATG . GGCCAGGAA . TGCCAAGGAG . 1260

1261 ACATCTATGC . ACGACCTTGG . GAAATGAGTT . GATGTCTCGG . GTAAACACC . GGAGACTAAT . 1320

1321 TCCTGCCCTG . CCCAATTTTG . CAGGGAGCAT . GGCTGTGAGG . ATGGGGTGAA . CTCACGCACA . 1380

1381 GCCAAGGACT . CCAAAATCAC . AACAGCATTG . CTGTTCTTAT . TTGCTGCCAC . ACCTGAGCCA . 1440

1441 GCCTGCTCCT . TCCCAGGAGT . GGAGGAGGCC . TGGGGGGAGG . GAGAGGAGTG . ACTGAGCTTC . 1500

1501 CCTCCCGTGT . GTTCTCOGTC . CCGCCCCAG . CAAGACAAGT . TAGATCTCCA . GGAGAACTGC . 1560

1561 CATCCAGCTT . TGGTGCAATG . GCTGAGTGCA . CAAGTGAGTT . GTTGCCCTGG . GTTCTCTTAA . 1620

1621 TCTATTACGC . TAGAACTTTG . AAGGACAATT . TCTTGCCATTA . ATAAAGGTTA . AGCCCTGAGG . 1680

1681 GGTCCCTGAT . AACAACTTGG . AGACCAGGAT . TTTATGGCTC . CCTCACTGA . TGGACAAGGA . 1740

1741 GGTCTGTGCC . AAAGAAGAAT . CCAATAAGCA . CATATTGAGC . ACTTGCTGTA . TATGCGATAT . 1800

1801 TGAGCACTGT . AGGCAAGACC . CAAGAAAGAG . AAGGAGCCAT . CTCCATCTTG . AAGGAATCA . 1860

1861 AAGACTCAAG . TGGGAACGAC . TGGGCACTGC . CACCACCAGA . AAGCTGTTGG . ACGAGACGGT . 1920

1921 CGAGCAGGGT . GCTGTGGGTG . ATATGGACAG . CAGAAGGGGG . AGACCAAGGT . TCCAGCTCAA . 1980

1981 CCAATAACTA . TTGCACAACC . ACCTGTCCCT . GCCTCAGTTC . CCTTTTATGT . AACATGAAGT . 2040

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Figure 6C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAAGCAA AGGGTGCTAC 2100
 2101 GTACATGTGA GGCATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160
 2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGSCGGTGTG 2220
 2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280
 2281 CCACCTGAG GCCCAACCG CCACACACAC AGGAGCATTT GGAGAGAAGC CCATGTCTTC 2340
 2341 AAGTCTGAT TTGTGATGAG CGAGAGGAAG ATATTCTTAA TCGGTCTTGC CCAGAGGATC 2400
 2401 ACAGTGCTGA GACCCCCAC CACCAGCCGG TACCTGGGAA GGGGAGAGT GCAGGCCTGC 2460
 2461 TCAGGGACTG TTCTGTCTC AGCAACCAAG GGATTGTTC TGTCATCAA TGTTTATTG 2520
 2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580
 2581 TCGGCAGTGC CAGGCAGCA CTCATTCACT TGATAAATGA ATATTTATTA GCTGGTTGGA 2640
 2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAAC TAGAAC CTGGAGGCT AGAACCTGGA 2700
 2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760
 2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGCTGGAA TCTGAAGGC TAGAACCTGG 2820
 2821 AGGGCTGGAA TCTGGAGGC TAGAACCTGG AGGCTAGAA CCTGGAGGC TAGAACCTAG 2880
 2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940
 2941 GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000
 3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060
 3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGCAGGCT AGAACCTGAC AAGCTAGAAC 3120
 3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAATG AGAAAAATTT ACATGGCAAA 3180
 3181 GAGCCATAA ATCCTGACCA ATCCAACCTT GAATTTTAAA GCAAAAGCGT GAAAAAAAG 3240

Figure 6D

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3241 ATTCCTCCTTACCCCCAAC CCACTCTTTT TTCCCACCAC CCACCTCTCCT CTGCCTCAGT 3300
3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAG AAGAAGTAA AACCATTTAG TATTAGTATT 3360
3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAG AGGCTGTGTT 3420
3421 TTGTCACACA GGGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCCTGAGAC TCTCTTAGGA 3480
3481 GCAGAGCTCT GCGCAATGG CCAATGTGGG ATCCACACCT GGTCCTGAGG GCAACTGAGT 3540
3541 CTGCGGGAGA AGAGCGGCC TATGCATGGT GTAGATGCC TGATAAAGAA CATCTGTCCT 3600
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTTACATC CAAACGAGAA 3660
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720
3721 AAAAAAAAAA AAA 3733

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Figure 7A

1 AATTCAGAGC CACCGCGGGC AGCGGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60
 61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCCA TAAAAAGCCT TCCACCCTCC TGTCTGCTTT 120
 121 AGAAGGAGCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTGTGTAT 180
 181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGACTCAGAC 240
 1 M D N V L P V D S D 10
 241 CTCTCCCCAA ACATCTCCAC TAACAACCTCG GAACCCCAATC AGTTCGTGCA ACCAGCCTGG 300
 11 L S P N I S T N T S E P N Q F V Q P A W 30
 301 CAAATGTGCC TTTGGGCAGC TGCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360
 31 Q I V L W A A A Y T V I V V T S V V G N 50
 361 GTGGTAGTGA TGTGGATCAT CTAGCCCCAC AAAAGAATGA GGACAGTGAC GAACTATTIT 420
 51 V V V M W I I L A H K R M R T V T N Y F 70
 421 CTGTTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACCTC 480
 71 L V N L A F A E A S M A A F N T V V N F 90
 481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCTGTCTCT ACTGCAAGTT CCACAACTTC 540
 91 T Y A V H N E W Y Y G L F Y C K F H N F 110
 541 TTTCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGTATAG 600
 111 F P I A A V F A S I Y S M T A V A F D R 130
 601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAG CCACAGCCAC CAAAGTGCTC 660
 131 Y M A I I H P L Q P R L S A T A T K V V 150
 661 ATCTGTGTCA TCTGGGTCTT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTACTCAACC 720
 151 I C V I W V L A L L L A F P Q G Y Y S T 170
 721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780
 171 T E T M P S R V V C M I E W P E H P N K 190
 781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGTGTA TCTACTTCCT CCCCTGCTG 840
 191 I Y E K V Y H I C V T V L I Y F L P L L 210
 841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGG 900
 211 V I G Y A Y T V V G I T L W A S E I P G 230
 901 GACTCTCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960
 231 D S S D R Y H E Q V S A K R K V V K M M 250

Figure 7B

961 ATTGTGCTGG TGTGCACCTT CGCATCTGCG TGGCTGCGCTT TCCACATCTT CTTCCTCCTG 1020
 251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080
 271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140
 291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCCTGC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200
 311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
 331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAGCGGCC TGGAGCCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320
 351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCGTCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
 371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440
 391 D S K T M T E S F S F S S N V L S * 407

1441 GGGCCTTTGG CAGGTGCAGC CCCCACTGCC TTTGACCTGC CTCCTTTCAT GCATGGAAT 1500

1501 TCCCTTCATC TGGAAACATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTC ATCCTTGAGT CAAAAAATCT CAATTCTTCC CTATCTTTGC 1620

1621 CACCCTCATG CTGTGTGACT CAAACCAAAAT CACTGAACCT TGCTGAGCCT GTAAAAATAA 1680

1681 AGGTCGGACC AGCTTTTCCT CAAGAGCCCA ATGCATTCCA TTCTGGAAG TGACTTTGGC 1740

1741 TGCATCGGAG TGCTCATTTT AGGATG 1766

Figure 8A

1 AATTCAGAGC CACCGCGGCG AGCGCGGCGAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60
 61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCCA TAAAAAGCCT TCCACCCTCC TGCTGCTTT 120
 121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180
 181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAAGC TCCTCCCGGT GGACTCAGAC 240
 1 M D N V L P V D S D 10
 241 CTCTCCCAAC ACACTCTCCAC TAACACCTCG GAACCCCAAT AGTTCGTGCA ACCAGCCTGG 300
 11 L S P N I S T N T S E P N Q F V Q P A W 30
 301 CAAATGTGCC TTTGGGCGAG TGCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360
 31 Q I V L W A A A Y T V I V V T S V V G N 50
 361 TGGTAGTGA TGTGGATCAT CTTAGCCAC AAAAGAATGA GGACAGTGAC GAACTATTT 420
 51 V V V M W I I L A H K R M R T V T N Y F 70
 421 CTGGTAACCG TGGCCTTCGC GGAGCCCTCC ATGGCTGCAT TCAATACAGT GGTGAACCTC 480
 71 L V N L A F A E A S M A A F N T V V N F 90
 481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCTGTCTCT ACTGCAAGTT CCACRACTTC 540
 91 T Y A V H N E W Y Y G L F Y C K F H N F 110
 541 TTCCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGTAGG 600
 111 F P I A A V F A S I Y S M T A V A F D R 130
 601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTGAG CCACAGCCAC CAAAGTGGTC 660
 131 Y M A I I H P L Q P R L S A T A T K V V 150
 661 ATCTGTGTCA TCTGGGTCCT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTACTCAACC 720
 151 I C V I W V L A L L L A F P Q G Y Y S T 170
 721 ACAGAGACCA TGCCCGAGAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780
 171 T E T M P S R V V C M I E W P E H P N K 190
 781 ATTTATGAGA AAGGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCTGCTG 840
 191 I Y E K V Y H I C V T V L I Y F L P L L 210
 841 GTAGTTGGCT ATGCATACAC CGTAGTGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900
 211 V I G Y A Y T V V G I T L W A S E I P G 230
 901 GACTCTCTGCT ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAATGATG 960
 231 D S S D R Y H E Q V S A K R K V V K M M 250

Figure 8B

961 ATTGTCGTGG TGTGCACCTT GCACATCTGC TGGCTGCCCT TCCACATCTT CTCCTCCTG 1020
 251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080
 271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCAATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140
 291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTCCGCTC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200
 311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
 331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAGCGGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320
 351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCGTCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
 371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440
 391 D S K T M T E S F S F S S N V L S * 407

1441 GGGCCTTTGG CAGGTGCAGC CCCCACTGCC TTTGACCTGC CTCCTTCAT GCATGGAAT 1500
 1501 TCCCTTCATC TGGAAACATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATCC ATCCTTGAGT CAAAAAATCT CAATTCTTCC CTATCTTTGC 1620
 1621 CACCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACCT TGCTGAGCT GTAAATATA 1680

1681 AGGTCGGACC AGCTTTTCCT CAAGAGCCCA ATGCATTCCT TTCTGGAAG TGACTTTGGC 1740
 1741 TGCATCGGAG TGCTCATTTT AGGATG 1766

Figure 9A

1 AATTCAGAGC CACCGGGGCG AGGCGGGGCG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60
 61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCCA TAAAAAGCCT TCCACCCCTC TGCTGCTTTT 120
 121 AGAAGSACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180
 181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGTG GGA CTGAGC 240
 1 M D N V L P V D S D 10
 241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTTCGTGCA ACCAGCCTGG 300
 11 L S P N I S T N T S E P N Q F V Q P A W 30
 301 CAAATGTGCC TTGCGGAGC TGCCTACAG GTCATGTGCG TGACCTCTGT GGTGGGCAAC 360
 31 Q I V L W A A A Y T V I V V T S V V G N 50
 361 GTGGTAGTGA TGTGGATCAT CTTAGCCAC AAAAGAATGA GGACAGTGAC GAACTATTTT 420
 51 V V V M W I I L A H K R M R T V T N Y F 70
 421 CTGTGTGAACC TGGCCTTCGC GGAGGCCCTCC ATGGCTGCAT TCAATACAT GOTGA ACTTC 480
 71 L V N L A F A E A S M A A F N T V V N F 90
 481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACA ACTTC 540
 91 T Y A V H N E W Y Y G L F Y C K F H N F 110
 541 TTTCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600
 111 F P I A A V F A S I Y S M T A V A F D R 130
 601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAG CCACAGCCAC CAAAGTGGTC 660
 131 Y M A I I H P L Q P R L S A T A T K V V 150
 661 ATCTGTGTCA TATGGGTCTT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTACTCAACC 720
 151 I C V I W V L A L L L A F P Q G Y Y S T 170
 721 ACAGAGACCA TGCCCGAGAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780
 171 T E T M P S R V V C M I E W P E H P N K 190
 781 ATTTATGAGA AAGTGTACCA CATCTGFTG ACTGTGCTGA TCTACTTCCT CCCCTGCTG 840
 191 I Y E K V Y H I C V T V L I Y F L P L L 210
 841 GTGATTTGGCT ATGCATACAC CGTAGTGGGA ATCACAATAT GGGCCAGTGA GATCCCCGGG 900
 211 V I G Y A Y T V V G I T L W A S E I P G 230
 901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAATGATG 960
 231 D S S D R Y H E Q V S A K R K V V K M M 250

Figure 9B

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961 ATTGTCGTGG TGTGCACCTT GGCATCTGCG TGGCTGCGCT TCCACATCTT CTCTCTCCTG 1020
251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGCCCATC 1080
271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140
291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCGGTC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200
311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAGCGGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320
351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCGTCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440
391 D S K T M T E S F S F S S N V L S * 407

1441 GGGCCTTTGG CAGGTGCAGC CCCCACTGCC TTTGACCTGC CTCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGGAAACATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAATCT CAATTCTTCC CTATCTTTGC 1620

1621 CACCTTCATG CTGTGTGACT CAAACCAAAT CACTGAACIT TGCTGAGCTT GTAAAAATAA 1680

1681 AGGTCGGACC AGCTTTTCTT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCAATGCGAG TGCTCATTTT AGGATG 1766

```


Figure 10A

1 AATTCAGAGC CACCGCGGC AGCGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60
 61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCCA TAAAAGCCT TCCACCCTCC TGTCTGCTTT 120
 121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTGTGTGA 180
 181 CAGATAGTAG GCTTTACGCC TAGCTTGGAA ATGGATAAGC TCCTCCCGGT GGACTCAGAC 240
 1 M D N V L P V D S D 10
 241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAAAT AGTTCGTGCA ACCAGCCTGG 300
 11 L S P N I S T N T S E P N Q F V Q P A W 30
 301 CAAATGTGCC TTGGGGCAGC TGCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360
 31 Q I V L W A A A Y T V I V V T S V V G N 50
 361 TTGGTAGTGA TGTGGATCAT CTTAGCCAC AAAAGAATGA GGACAGTGAC GAACTATTTT 420
 51 V V V M W I I L A H K R M R T V T N Y F 70
 421 TTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACCTC 480
 71 L V N L A F A E A S M A A F N T V V N F 90
 481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACACTTTC 540
 91 T Y A V H N E W Y Y G L F Y C K F H N F 110
 541 TTTCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGTATAG 600
 111 F P I A A V F A S I Y S M T A V A F D R 130
 601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTGAG CCACAGCCAC CAAAGTGTC 660
 131 Y M A I I H P L Q P R L S A T A T K V V 150
 661 ATCTGTGTCA TCTGGGTCCT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTACTCAAC 720
 151 I C V I W V L A L L L A F P Q G Y Y S T 170
 721 ACAGAGACCA TGCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780
 171 T E T M P S R V V C M I E W P E H P N K 190
 781 ATTTATGAGA AAGGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCTGCTG 840
 191 I Y E K V Y H I C V T V L I Y F L P L L 210
 841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGG 900
 211 V I G Y A Y T V V G I T L W A S E I P G 230
 901 GACTCTCTCT ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGTGGT CAAATGATG 960
 231 D S S D R Y H E Q V S A K R K V V K M M 250

Figure 10B

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961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTTCCTCCTG 1020
251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080
271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140
291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCGGTC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200
311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320
351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCATCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440
391 D S K T M T E S F S F S S N V L S * 407

1441 GGGCCTTTGG CAGGTGCAGC CCCCACCTGC TTTGACCTGC CTCCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGGAAACATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAATCT CAATTCCTCC CTATCTTTGC 1620

1621 CACCCCTATG CTGTGTGACT CAAACCAAAAT CACTGAACIT TGCTGAGCCT GTAAAAATAA 1680

1681 AGGTCGGACC AGCTTTTCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGSC 1740

1741 TGCAATCGAG TGCTCATTTT AGGATG 1766

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Figure 11A

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1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCGCGCCAG 60
61 ATGGCCTCCA GGCTGACCCT GCTGACCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
1 M A S R L T L L T L L L A G D R A 20
121 TCCTCAAATC CAAATGCTAC CAGTCCAGC TCCAGGATC CAGAGAGTTT GCAAGACAGA 180
21 S S N P N A T S S S S Q D P E S L Q D R 40
181 GCGCAAGGGA AGGTGCGAAC AACAGTTATC TCCAAGATGC TATTCGTTGA ACCCATCTTG 240
41 G E G K V A T T V I S K M L F V E P I L 60
241 GAGGTTTCCA GCTTGGCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
61 E V S S L P T T N S T T N S A T K I T A 80
301 AATACCACCTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCAA ACCCACCATG 360
81 N T T D E P T T Q P T T E P T T Q P T I 100
361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
101 Q P T Q P T T Q L P T D S P T Q P T T G 120
421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
121 S F C P G P V T L C S D L E S H S T E A 140
481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCTTT CTCAGCAATG 540
141 V L G D A L V D F S L K L Y H A F S A M 160
541 AAGAAAGTGG AGACCAACAT GGCCTTTTCC CCATTCAAGA TCGCCAGCCT CTTTACCAG 600
161 K K V E T N M A F S P F S I A S L L T Q 180
601 GTCCTGCTCG GGGCTGGGCA GAACACCAAA ACAAACTGG AGAGCATCCT CTCTTACCCC 660
181 V L L G A G Q N T K T N L E S I L S Y P 200
661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTACCTCA 720
201 K D F T C V H Q A L K G F T T K G V T S 220
721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
221 V S Q I F H S P D L A I R D T F V N A S 240
781 CGGACCCGTG ACAGCAGCAG CCCCAGATC CTAAGCAACA ACAGTAGCAG CAACTTGGAG 840
241 R T L Y S S S P R V L S N N S D A N L E 260
841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAAACAAG TCAGCCGGGT GCTAGACAGT 900
261 L I N T W V A K N T N N K I S R L L D S 280
901 CTGCGCTCCG ATACCCCGCT TGTCTCTCTC AATGCTATCT ACCTGAGTGC CAAGTGAAG 960
281 L P S D T R L V L L N A I Y L S A K W K 300

```

Figure 11B

961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCCTTC ACTTCAAAAA CTCAGTTATA 1020
 301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCAATGA CCAAACCTTG 1080
 321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGTGACCC 1140
 341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATGCTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTCCTCAAG 1200
 361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCCTCTAAC ACTACCCCGC 1260
 381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAATGGA ATTCTTCGAT 1320
 401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCCTAACCT GTGTGGGCTG ACAGAGSACC CAGATCTTCA GGTTCCTGCG 1380
 421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAAGTGACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
 441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500
 461 A I S V A R T L L V F E V Q Q P F L F V 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
 481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCTCAGC TGTCGGCTAT 1680

1681 CCACCAAAAG GSCCTCTGAG GGTCTGGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTT TCGAGTTTCT CTAGTTCAAG TTCACGAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

Figure 12A

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1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCCGCCAG 60
61 ATGGCCTCCA GGCTGACCTT GCTGACCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
1 M A S R L T L L T L L L L A G D R A 20
121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCAGGATC CAGAGAGTTT GCAAGACAGA 180
21 S S N P N A T S S S S Q D P E S L Q D R 40
181 GCGCAAGGGA AGGTGCGAAC AACAGTTATC TCCAAGATGC TATTCGTTGA ACCATCCTG 240
41 G E G K V A T T V I S K M L F V E P I L 60
241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
61 E V S S L P T T N S T T N S A T K I T A 80
301 AATACCACCTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCA ACCCACCCT 360
81 N T T D E P T T Q P T T E P T T Q P T I 100
361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
101 Q P T Q P T T Q L P T D S P T Q P T T G 120
421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
121 S F C P G P V T L C S D L E S H S T E A 140
481 GTGTTGGGGG ATGCTTTGGT AGATTCTCTC CTGAAGCTCT ACCACGCCTT CTCAGCAATG 540
141 V L G D A L V D F S L K L Y H A F S A M 160
541 AAGAAGGTGG AGACCAACAT GGCCTTTTCC CCATTTCAGA TCGCCAGCCT CCTTACCCAG 600
161 K K V E T N M A F S P F S I A S L L T Q 180
601 GTCTCTGCTG GGGCTGGGCA GAACACCAAA ACAACCTGG AGAGCATCCT CTCTTACCCC 660
181 V L L G A G Q N T K T N L E S I L S Y P 200
661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTACCTCA 720
201 K D F T C V H Q A L K G F T T K G V T S 220
721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
221 V S Q I F H S P D L A I R D T F V N A S 240
781 CGGACCTCTG ACAGCAGCAG CCCAGAGTTC CTAAGCAACA ACAGTGAGCC CAACTTGGAG 840
241 R T L Y S S S P R V L S N N S D A N L E 260
841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACACAAGA TCAGCCGGCT GCTAGACAGT 900
261 L I N T W V A K N T N N K I S R L L D S 280
901 CTGCCCTCCG ATACCCGCCT TGTCTCTCTC AATGCTATCT ACCTGAGTGC CAAGTGAAG 960
281 L P S D T R L V L L N A I Y L S A K W K 300

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Figure 12B

961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCCTTC ACTTCAAAAA CTCAGTTATA 1020
 301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCAATTGA CCAAACTTTG 1080
 321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140
 341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTTCAAG 1200
 361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCCTCTAAC ACTACCCCGC 1260
 381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAGTGA CGACCACTCA GGATATGCTC TCAATCATGG AGAAATGGA ATCTCTCGAT 1320
 401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTCCTGCG 1380
 421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAAC TGACA GAGACTGGG TGGAGGCGGC TGCAGCCTCC 1440
 441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500
 461 A I S V A R T L L V F E V Q Q P F L F V 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
 481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCTGCCT GGACTTGCCG CTGCCACCTC CTGCCTCAGC TGTCGGCTAT 1680

1681 CCACCAAAAG GGCCTCTGAG GGTCTGGGCA AGGGACCTGC TTCTATTAGC OCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

Figure 13A

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1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGSAGT CCGCTGACGT CGCCGCCAG 60
61 ATGGCCTCCA GGCTGACCTT GCTGACCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
1 M A S R L T L L T L L L L A G D R A 20
121 TCCTCAAATC CAAATGCTAC CAGTCCAGC TCCAGGATC CAGAGAGTTT GCAAGACAGA 180
21 S S N P N A T S S S S Q D P E S L Q D R 40
181 GCGCAAGGGA AGGTGCGAAC AACAGTTATC TCCAAGATGC TATTCGCTGA ACCCATCTTG 240
41 G E G K V A T T V I S K M L F A E P I L 60
241 GAGGTTTCCA GCTTGGCCAG AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
61 E V S S L P T T N S T T N S A T K I T A 80
301 AATACCACCTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCA ACCCACCATC 360
81 N T T D E P T T Q P T T E P T T Q P T I 100
361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
101 Q P T Q P T T Q L P T D S P T Q P T T G 120
421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
121 S F C P G P V T L C S D L E S H S T E A 140
481 GTGTTGGGGG ATGCTTTGGT AGATTCTCC CTGAAGCTCT ACCACGCCTT CTCAGCAATG 540
141 V L G D A L V D F S L K L Y H A F S A M 160
541 AAGAAGTGG AGACCAACAT GGCCTTTTCC CCATTCAGCA TCGCCAGCCT CCTTACCAG 600
161 K K V E T N M A F S P F S I A S L L T Q 180
601 GTCCTGCTCG GGGCTGGGCA GAACACCAAA ACAACCTGG AGAGCATCCT CTCTTACCCC 660
181 V L L G A G Q N T K T N L E S I L S Y P 200
661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAGG TGTCACCTCA 720
201 K D F T C V H Q A L K G F T T K G V T S 220
721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
221 V S Q I F H S P D L A I R D T F V N A S 240
781 CGGACCTGTT ACAGCAGCAG CCCCAGAGTC CTAAGCACA ACAGTGACGC CAACTTGGAG 840
241 R T L Y S S S P R V L S N N S D A N L E 260
841 CTCATCAACA CCTGGGTGTC CAAGAACACC AACACAAGA TCAGCCGGT GCTAGACAGT 900
261 L I N T W V A K N T N N K I S R L L D S 280
901 CTGCCCTCCG ATACCCGCCT TGTCTCTCTC AATGCTATCT ACCTGAGTGC CAAGTGGAG 960
281 L P S D T R L V L L N A I Y L S A K W K 300

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Figure 13B

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961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020
301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCAATTGA CCAAACTTTG 1080
321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140
341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTCCTAAG 1200
361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC 1260
381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAATGA CGACAGGCCA GGAATATGCTC TCAATCATGG AGAAATGGA ATTCCTCGAT 1320
401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTCCTGCG 1380
421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAAGTGACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTGGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500
461 A I S V A R T L L V F E V Q Q P F L F V 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCAGGGCCC 1560
481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTC 1620

1621 AGCCCCIGCTG CTGCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCTCAGC TGTCGGCTAT 1680

1681 CCACCAAAAG GGCCTCTGAG GGTCTGGCCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

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Figure 14A

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1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCCGCCAG 60
61 ATGGCCTCCA GSGTGACCTT GCTGACCTTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
1 M A S R L T L L T L L L L L A G D R A 20
121 TCCTCAAATC CAAATGCTAC CAGTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
21 S S N P N A T S S S S Q D P E S L Q D R 40
181 GGCGAAGGGA AGGTGCGAAC AACAGTTATC TCCAAGATGC TATTCGTTGA ACCCATCTGT 240
41 G E G K V A T T V I S K M L F V E P I L 60
241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
61 E V S S L P T T N S T T N S A T K I T A 80
301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCAA ACCCACCATC 360
81 N T T D E P T T Q P T T E P T T Q P T I 100
361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
101 Q P T Q P T T Q L P T D S P T Q P T T G 120
421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
121 S F C P G P V T L C S D L E S H S T E A 140
481 GTGTTGGGGG ATGCTTTGGT AGATTCTTCC CTGAAGCTCT ACCAGCCTT CTCAGGAATG 540
141 V L G D A L V D F S L K L Y H A F S G M 160
541 AAGAAGGTGG AGACCAACAT GGCCTTTTCC CCATTACAGA TCGCCAGCCT CCTTACCCAG 600
161 K K V E T N M A F S P F S I A S L L T Q 180
601 GTCTCTCTCG GGGCTGGGCA GAACACCAAA ACAAACTTGG AGAGCATCTC CTCTTACCCC 660
181 V L L G A G Q N T K T N L E S I L S Y P 200
661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAAG TGTCACCTCA 720
201 K D F T C V H Q A L K G F T T K G V T S 220
721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCNTAAGGG ACACCTTTGT GAATGCCTCT 780
221 V S Q I F H S P D L A I R D T F V N A S 240
781 CGGACCTCTG ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTAGCAG CAACPTGGAG 840
241 R T L Y S S S P R V L S N N S D A N L E 260
841 CTCTATCAACA CCTGGGTGGC CAAGAACACC AACAACAAGA TCAGCCGGGT GCTAGACAGT 900
261 L I N T W V A K N T N N K I S R L L D S 280
901 CTGCCCTCCG ATACCCGCCT TGTCTCTCTC AATGCTATCT ACCTGAGTGC CAAGTGAAG 960
281 L P S D T R L V L L N A I Y L S A K W K 300

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Figure 14B

961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020
 301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCAATTGA CCAAACCTTG 1080
 321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGTGTACC 1140
 341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATGCTCT TGAAGACATG GAACAGSCTC TCAGCCCTTC TGTTCCTAAG 1200
 361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCTCTTAAC ACTACCCCGC 1260
 381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAATGGA ATTCTTCGAT 1320
 401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGSACC CAGATCTTCA GGTTCGTGCG 1380
 421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAAGTGACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
 441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500
 461 A I S V A R T L L V F E V Q Q P F L F V 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCAGGGGCC 1560
 481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCTCAGG TGTCGGCTAT 1680

1681 CCACCAAAAG GGCCTCTGAG GGTCTGSGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

Figure 15A

```

1  AGTCTGCACT  GGAGCTGCCT  GGTGACCAGA  AGTTTGGAGT  CCGCTGACGT  CGCCGCCAG  60

61  ATGGCCTCCA  GGCTGACCTT  GCTGACCCTC  CTGCTGCTGC  TGCTGGCTGG  GGATAGAGCC  120
1  M  A  S  R    L  T  L    L  T  L    L  L  L  L    L  A  G    D  R  A    20

121 TCCTCAAATC  CAAATGCTAC  CAGTCCAGC  TCCAGGATC  CAGAGAGTTT  GCAAGACAGA  180
21 S  S  N  P    N  A  T    S  S  S    S  Q  D  P    E  S  L    Q  D  R    40

181 GCGCAAGGGA  AGGTGCAAC  AACAGTTATC  TCCAAGATGC  TATTCGTTGA  ACCATCCTG  240
41 G  E  G  K    V  A  T    T  V  I    S  K  M  L    F  V  E    P  I  L    60

241 GAGGTTTCCA  GCTTGCCGAC  AACCAACTCA  ACAACCAATT  CAGCCACCAA  AATAACAGCT  300
61 E  V  S  S    L  P  T    T  N  S    T  T  N  S    A  T  K    I  T  A    80

301 AATACCACCTG  ATGAACCCAC  CACACAACCC  ACCACAGAGC  CCACCACCCA  ACCACCACCT  360
81 N  T  T  D    E  P  T    T  Q  P    T  T  E  P    T  T  Q    P  T  I    100

361 CAACCCACCC  AACCAACTAC  CCAGCTCCCA  ACAGATTCTC  CTACCCAGCC  CACTACTGGG  420
101 Q  P  T  Q    P  T  T    Q  L  P    T  D  S  P    T  Q  P    T  T  G    120

421 TCCTTCTGCC  CAGGACCTGT  TACTCTCTGC  TCTGACTTGG  AGAGTCATTC  AACAGAGGCC  480
121 S  F  C  P    G  P  V    T  L  C    S  D  L  E    S  H  S    T  E  A    140

481 GTGTTGGGGG  ATGCTTTGGT  AGATTCTCTC  CTGAAGCTCT  ACCACGCCTT  CTCAGCAATG  540
141 V  L  G  D    A  L  V    D  F  S    L  K  L  Y    H  A  F    S  A  M    160

541 AAGAAGTGG  AGACCAACAT  GGCCTTTTCC  CCATTACAGA  TCGCCAGCCT  CCTTACCCAG  600
161 K  K  V  E    T  N  M    A  F  S    P  F  S  I    A  S  L    L  T  Q    180

601 GTCCTGCTCG  GGGCTGGGCA  GAACACCAAA  ACAAACTGG  AGAGCATCCT  CTCTTACCCC  660
181 V  L  L  G    A  G  Q    N  T  K    T  N  L  E    S  I  L    S  Y  P    200

661 AAGACTTCA  CCTGTGTCCA  CCAGGCCCTG  AAGGCTTCA  CGACCAAGG  TGTACCTCA  720
201 K  D  F  T    C  V  H    Q  A  L    K  G  F  T    T  K  G    V  T  S    220

721 GTCTCTCAGA  TCTTCCACAG  CCCAGACCTG  GCCATAAGGG  ACACCTTTGT  GAATGCCTCT  780
221 V  S  Q  I    F  H  S    P  D  L    A  I  R  D    T  F  V    N  A  S    240

781 CGGACCTGT  ACAGCAGCAG  CCCCAGAGTC  CTAAGCAACA  ACAGTGAGCC  CAACTTGGAG  840
241 R  T  L  Y    S  S  S    P  R  V    L  S  N  N    S  D  A    N  L  E    260

841 CTCATCAACA  CCTGGGTGGC  CAAGAACACC  AACAACAAGA  TCAGCCGGCT  GCTAGACAGT  900
261 L  I  N  T    W  V  A    K  N  T    N  N  K  I    S  R  L    L  D  S    280

901 CTGCCCTCCG  ATACCCGCCT  TGTCTCTCTC  AATGCTATCT  ACCTGAGTGC  CAAGTGGAG  960
281 L  P  S  D    T  R  L    V  L  L    N  A  I  Y    L  S  A    K  W  K    300

```

Figure 15B

961 ACACATTTG ATCCCAAGAA AACCAGAATG GAACCTTTC ACTTCAAAAA CTCAGTTATA 1020
 301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCAATTGA CCAAACITTG 1080
 321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGCGAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140
 341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTTCAAG 1200
 361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC 1260
 381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAATGGA ATTCTTCGAT 1320
 401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGSACC CAGATCTTCA GGTTCCTCGG 1380
 421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAAGTGACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
 441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCATG 1500
 461 A I S V A R T L L V F E V Q Q P F L F M 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCAGGGGCC 1560
 481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCCTGCT GGACTTGCCC CTGCCACCTC CTGCCCTCAGC TGTCGGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

Figure 16

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1 TCCTCCACCT GCTGGCCCTT GGACACCTCT GTCACCATGT GGTTCCTGTT TCTGTGCCTC 60
1 M W F L V L C L 8

61 CCCTGTGCCC TGGGGGGGAC TGGTGCTGCG CCCCGGATTC AGTCCCGGAT TGTGGGAGGC 120
9 A L S L G G T G A A P P I Q S R I V G G 28

121 TGGGAGTGTG AGCAGCATTC CCAGCCCTGG CAGGCGGCTC TGTACCATTT CAGCACTTTC 180
29 W E C E Q H S Q P W Q A A L Y H F S T F 48

181 CAGTGTGGGG GCATCCTGTT GCACCCGAG TGGTGCTCTA CAGCTGCTCA TTGCATCAGC 240
49 Q C G G I L V H R Q W V L T A A H C I S 68

241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTGTT ACGACGAAA CACAGCCGAG 300
69 D N Y Q L W L G R H N L F D D E N T A Q 88

301 TTTGTTCATG TCAGTGAGAG CTTCACACAC CCTGGCTTCA ACATGAGCCT CCTGGAGAAC 360
89 F V H V S E S F P H P G F N M S L L E N 108

361 CACACCCGCC AAGCAGAAGA GGAATACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420
109 H T R Q A D E D Y S H D L M L L R L T E 128

421 CCTGTGATGA CCATCACAGA TGCTGTGAAG GTCGTGGAGT TGCCCAACGA GGAACCCGAA 480
129 P A D T I T D A V K V V E L P T E E P E 148

481 GTGGGGAGCA CCTGTTTGGC TTCCGGCTGG GGCAGCATCG AACCAGAGAA TTCTCATTTT 540
149 V G S T C L A S G W G S I E P E N F S F 168

541 CCAGATGATC TCCAGTGTGT GGACCTCAAA ATCTCGCTTA ATGATGAGTG CAAAAAGGC 600
169 P D D L Q C V D L K I L P N D E C K K A 188

601 CACGTCCAGA AGGTGACAGA CTTCATGCTG TGTGTGGGAC ACCTGGAAGG TGGCAAAGAC 660
189 H V Q K V T D F M L C V G H L E G G K D 208

661 ACCTGTGTGG GTGATTCAGG GGGCCCGCTG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720
209 T C V G D S G G P L M C D G V L Q G V T 228

721 TCATGTGGGT ACGTCCCTTG TGGCACCCCT AATAAGCCTT CTGTGCGCCT CAGAGTGCTG 780
229 S W G Y V P C G T P N K P V A V R V L 248

781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840
249 S Y V K W I E D T I A E N S * 262

841 CCCTACCCCC AGTAAAAACA AATGTGCATC C 871

```

Figure 17

1 TCCTCCACCT GCTGCCCCCT GGACACCTCT GTCACCATGT GGTTCCTGGT TCTGTGCCTC 60
 1 M W F L V L C L 8
 61 GCCTGTGCCC TGGGGGGGAC TGGTGCTGCG CCCCAGATTG AGTCCCGGAT TGTGGGAGGC 120
 9 A L S L G G T G A A P P I Q S R I V G G 28
 121 TGGGAGTGTG AGCAGCATTC CCAGCCCTGG CAGGCGGCTC TGTACCATTG CAGCACTTTC 180
 29 W E C E Q H S Q P W Q A A L Y H F S T F 48
 181 CAGTGTGGGG GCATCCTGGT GCACCGCCAG TGGGTGCTCA CAGCTGCTCA TTGCATCAGC 240
 49 Q C G G I L V H R Q W V L T A A H C I S 68
 241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTGTG ACGACGAAAA CACAGCCGAG 300
 69 D N Y Q L W L G R H N L F D D E N T A Q 88
 301 TTTGTTTCATG TCAGTGAGAG CTTCACACAC CCTGGCTTCA ACATGAGCCT CCTGAGAAAC 360
 89 F V H V S E S F P H P G F N M S L L E N 108
 361 CACACCCGCC AAGCAGACGA GGACTACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420
 109 H T R Q A D E D Y S H D L M L L R L T E 128
 421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTCGTGGAGT TGCCCCACGA GGAACCCGAA 480
 129 P A D T I T D A V K V V E L P T E E P E 148
 481 GTGGGGAGCA CCTGTTTGGC TTCCGGCTGG GGCAGCATCG AACCAGAGAA TTTCTCATTT 540
 149 V G S T C L A S G W G S I E P E N F S F 168
 541 CCAGATGATC TCCAGTGTGT GGACCTCAAA ATCCTGCCTA ATGATGAGTG CGAAAAAGCC 600
 169 P D D L Q C V D L K I L P N D E C E K A 188
 601 CACGTCCAGA AGGTGACAGA CTTCATGCTG TGTGTCGGAC ACCTGGAAGG TGCCAAAGAC 660
 189 H V Q K V T D F M L C V G H L E G G K D 208
 661 ACCTGTGTGG GTGATTGAGG GGGCCCGCTG ATGTGTGATG GTGTGCTCCA AGGTGTGACA 720
 209 T C V G D S G G P L M C D G V L Q G V T 228
 721 TCATGGGGCT ACGTCCCTTG TGGCACCCGC AATAAGCCCT CTGTGCGCTG CAGAGTGTCT 780
 229 S W G Y V P C G T P N K P S V A V R V L 248
 781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAAGT CCTGAACGGC CAGCCCTGTC 840
 249 S Y V K W I E D T I A E N S * 262
 841 CCCTACCCCC AGTAAAAATCA AATGTGCATC C 871

Figure 18

1 TCCTCCACCT GCTGCCCCCT GGACACCTCT GTCACCATGT GGTTCCTGGT TCTGTGCCTC 60
 1 M W F L V L C L 8
 61 GCCCTGTCCC TGGGGGGGAC TGGTGTCTGG CCCCAGATTC AGTCCCAGAT TGTGGGAGGC 120
 9 A L S L G G T G A A P P I Q S R I V G G 28
 121 TGGGAGTGTG AGCAGCATTC CCAGCCCTGG CAGGCGGCTC TGTACCATT T CAGCACTTTC 180
 29 W E C E Q H S Q P W Q A A L Y H F S T F 48
 181 CAGTGTGGGG GCATCCTGGT GCACCGCCAG TGGGTGCTCA CAGCTGCTCA TTGCATCAGC 240
 49 Q C G G I L V H R Q W V L T A A H C I S 68
 241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTGTTG ACGACGAAAA CACAGCCCAG 300
 69 D N Y Q L W L G R H N L F D D E N T A Q 88
 301 TTTGTTCATG TCAGTGAGAG CTTCACACAC CCTGGCTTCA ACATGAGCCT CCTGAGAGAC 360
 89 F V H V S E S F P H P G F N M S L L E N 108
 361 CACACCCGCC AAGCAGACGA GGACTACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420
 109 H T R Q A D E D Y S H D L M L L R L T E 128
 421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTCGTGGAGT TGCCCCACCA GGAACCCGAA 480
 129 P A D T I T D A V K V V E L P T Q E P E 148
 481 GTGGGGAGCA CCTGTTTGGC TTCCGGCTGG GGCAGCATCG AACCAGAGAA TTTCTCATTT 540
 149 V G S T C L A S G W G S I E P E N F S F 168
 541 CCAGATGATC TCCAGTGTGT GGACCTCAAA ATCCTGCCTA ATGATGAGTG CAAAAAGCC 600
 169 P D D L Q C V D L K I L P N D E C K K A 188
 601 CACCTCCAGA AGGTGACAGA CTTCATGCTG TGTGTGGAC ACCTGGAAGG TGGCAAAGC 660
 189 H V Q K V T D F M L C V G H L E G G K D 208
 661 ACCTGTGTGG GTGATTGAGG GGGCCCGCTG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720
 209 T C V G D S G G P L M C D G V L R G V T 228
 721 TCATGGGGCT ACGTCCCTTG TGGCACCCCC AATAAGCCTT CTGTGCGCGT CAGAGTGTGT 780
 229 S W G Y V P C G T P N K P V A V R V L 248
 781 TCTTATGTGA AGTGGATCGA GGACACCATTA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840
 249 S Y V K W I E D T I A E N S * 262
 841 CCCTACCCCC AGTAAAAATCA AATGTGCATC C 871

Figure 19

BRB1_MOUSE MASQASLQLPSNQSQAPPNITSCGAPAEAWDLLQVLPFGKITICFFGLLGNNLVLS
 BRB1_RAT MASEVLLELOPSNRSLOAPNITSCESALFEWDDLQVLPFGKITICFFGLLGNNLVLS
 BRB1_HUMAN MASSWHPLELOSNQSQLEFNDACDAPAEAWDLLHRVLPITITISICFFGLLGNNLVLS
 BRB1_RABIT MASQASLPLELOPSNQSQAPPNATSCGALFEWDDLHRVLPITITITITLGLLGNNLVLS

BRB1_MOUSE FFLLPWTRWV...QRRRLTLEIYLANLAASDLVFVLGLPFWAENGNNFNNWPFQSDI
 BRB1_RAT FFLLPWTRWV...QRRRLTLEIYLANLAASDLVFVLGLPFWAENGNNFNNWPFQSDI
 BRB1_HUMAN VFLLP.....RRQLNLEIYLANLAASDLVFVLGLPFWAENGNNFNNWPFQALL
 BRB1_RABIT VFLLA.....RRQLNLEIYLANLAASDLVFVLGLPFWAENGNNFNNWPFQALL

BRB1_MOUSE CRVVSQVIKANLFISIFLVVAISQDRYRLVYPMISWGRRRRRQAQVTCLLIIVAGGLLS
 BRB1_RAT CRVVSQVIKANLFISIFLVVAISQDRYRLVYPMISWGRRRRRQAQVTCLLIIVAGGLLS
 BRB1_HUMAN CRVVSQVIKANLFISIFLVVAISQDRYRLVYPMISWGRRRRRQAQVTCLLIIVAGGLLS
 BRB1_RABIT CRVVSQVIKANLFISIFLVVAISQDRYRLVYPMISWGRRRRRQAQVTCLLIIVAGGLLS

BRB1_MOUSE TPTFLLRSVKQVVDLNNISACILLPHEAWHFARMVELNVLGFLPLAAILFFNYHILASL
 BRB1_RAT TPTFLLRSVKQVVDLNNISACILLPHEAWHFARMVELNVLGFLPLAAILFFNYHILASL
 BRB1_HUMAN TPTFLLRSVKQVVDLNNISACILLPHEAWHFARMVELNVLGFLPLAAILFFNYHILASL
 BRB1_RABIT TPTFLLRSVKQVVDLNNISACILLPHEAWHFARMVELNVLGFLPLAAILFFNYHILASL

*

BRB1_MOUSE RGCKEASRTRCGGPKGSKTGLILTLVASFLVCWAPYHFFAFLEFLVQVRNIQDCFWKEI
 BRB1_RAT RGCKEASRTRCGGPKGSKTGLILTLVASFLVCWAPYHFFAFLEFLVQVRNIQDCFWKEI
 BRB1_HUMAN RTREESRTRVRGPKGSKTGLILTLVASFLVCWAPYHFFAFLEFLVQVRNIQDCFWKEI
 BRB1_RABIT RRRGERVPRCGGPKGSKTGLILTLVASFLVCWAPYHFFAFLEFLVQVRNIQDCFWKEI

*

BRB1_MOUSE TDLGLQLANFFAFVNSCLNPVIYVFGLEFTVWELGTL...
 BRB1_RAT TDLGLQLANFFAFVNSCLNPVIYVFGLEFTVWELGTL...
 BRB1_HUMAN TDLGLQLANFFAFVNSCLNPVIYVFGLEFTVWELGTL...
 BRB1_RABIT TDLGLQLANFFAFVNSCLNPVIYVFGLEFTVWELGTL...

BRB1_MOUSE ~~~~
 BRB1_RAT ~~~~
 BRB1_HUMAN FWRN
 BRB1_RABIT FWRN

Figure 20

```

BRB2_MOUSE ~~~~~MPCSMKLLGFVSVHE. PMPTAASFGIEFMFNITQVLGSAHNGTFSKDN. CPDTEW
BRB2_RAT   MDRRSSCLP. KTAQAVMAVFW. GPGCHLSTCIEMFNITQVLGSAHNGTFSKDN. CPDTEW
BRB2_RABIT ~~~~~MPCSMKLLGFVSVHE. PMPTAASFGIEFMFNITQVLGSAHNGTFSKDN. CPDTEW
BRB2_CAVPO ~~~~~MPCSMKLLGFVSVHE. PMPTAASFGIEFMFNITQVLGSAHNGTFSKDN. CPDTEW
BRB2_HUMAN ~~~~~MPCSMKLLGFVSVHE. PMPTAASFGIEFMFNITQVLGSAHNGTFSKDN. CPDTEW

BRB2_MOUSE WSNLNIQAPPLWVFLATLENIFVLVSVFCLHKSSCTVAETYLGNLAAADLILACGLPF
BRB2_RAT   WSNLNIQAPPLWVFLATLENIFVLVSVFCLHKSSCTVAETYLGNLAAADLILACGLPF
BRB2_RABIT WSNLNIQAPPLWVFLATLENIFVLVSVFCLHKSSCTVAETYLGNLAAADLILACGLPF
BRB2_CAVPO WSNLNIQAPPLWVFLATLENIFVLVSVFCLHKSSCTVAETYLGNLAAADLILACGLPF
BRB2_HUMAN WSNLNIQAPPLWVFLATLENIFVLVSVFCLHKSSCTVAETYLGNLAAADLILACGLPF

BRB2_MOUSE WAITIANNFDFLFGVLCRVVNTMIYMNLYSSICFLMLVSDIRYALVKTMSMGRMRGV
BRB2_RAT   WAITIANNFDFLFGVLCRVVNTMIYMNLYSSICFLMLVSDIRYALVKTMSMGRMRGV
BRB2_RABIT WAITIANNFDFLFGVLCRVVNTMIYMNLYSSICFLMLVSDIRYALVKTMSMGRMRGV
BRB2_CAVPO WAITIANNFDFLFGVLCRVVNTMIYMNLYSSICFLMLVSDIRYALVKTMSMGRMRGV
BRB2_HUMAN WAITIANNFDFLFGVLCRVVNTMIYMNLYSSICFLMLVSDIRYALVKTMSMGRMRGV

BRB2_MOUSE WAKLYSLVIWGCTLLSSPMLVFRTMKDYRDEGHNVTAACVITYPSRSWEVFTNVLNLVG
BRB2_RAT   WAKLYSLVIWGCTLLSSPMLVFRTMKDYRDEGHNVTAACVITYPSRSWEVFTNVLNLVG
BRB2_RABIT WAKLYSLVIWGCTLLSSPMLVFRTMKDYRDEGHNVTAACVITYPSRSWEVFTNVLNLVG
BRB2_CAVPO WAKLYSLVIWGCTLLSSPMLVFRTMKDYRDEGHNVTAACVITYPSRSWEVFTNVLNLVG
BRB2_HUMAN WAKLYSLVIWGCTLLSSPMLVFRTMKDYRDEGHNVTAACVITYPSRSWEVFTNVLNLVG

BRB2_MOUSE FLPLSLVITFCTVQIMQVLRNNEMOKFKKIQTERRATVLVLAVLLFVFCWLPFOISTPL
BRB2_RAT   FLPLSLVITFCTVQIMQVLRNNEMOKFKKIQTERRATVLVLAVLLFVFCWLPFOISTPL
BRB2_RABIT FLPLSLVITFCTVQIMQVLRNNEMOKFKKIQTERRATVLVLAVLLFVFCWLPFOISTPL
BRB2_CAVPO FLPLSLVITFCTVQIMQVLRNNEMOKFKKIQTERRATVLVLAVLLFVFCWLPFOISTPL
BRB2_HUMAN FLPLSLVITFCTVQIMQVLRNNEMOKFKKIQTERRATVLVLAVLLFVFCWLPFOISTPL

BRB2_MOUSE DTLRLRGVLSSGCWDEHIDVITQISSYAYSNSCLNPLVYVIVGKRFKKRSREYVYQICR
BRB2_RAT   DTLRLRGVLSSGCWDEHIDVITQISSYAYSNSCLNPLVYVIVGKRFKKRSREYVYQICR
BRB2_RABIT DTLRLRGVLSSGCWDEHIDVITQISSYAYSNSCLNPLVYVIVGKRFKKRSREYVYQICR
BRB2_CAVPO DTLRLRGVLSSGCWDEHIDVITQISSYAYSNSCLNPLVYVIVGKRFKKRSREYVYQICR
BRB2_HUMAN DTLRLRGVLSSGCWDEHIDVITQISSYAYSNSCLNPLVYVIVGKRFKKRSREYVYQICR

*
BRB2_MOUSE KGCSEPPVQOMENSMGTLRTSISVERQIHKLQDWAGK
BRB2_RAT   KGCSEPPVQOMENSMGTLRTSISVERQIHKLQDWAGK
BRB2_RABIT KGCSEPPVQOMENSMGTLRTSISVERQIHKLQDWAGK
BRB2_CAVPO KGCSEPPVQOMENSMGTLRTSISVERQIHKLQDWAGK
BRB2_HUMAN KGCSEPPVQOMENSMGTLRTSISVERQIHKLQDWAGK

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Figure 21A

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1 CTGTGCATGG CATCATCCTG GCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGTACAGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGTGCGCNA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTCT 180
39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCTGCCC CCGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAANGG GGTTCATCAAG 360
99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTGTG TCATCAGCAT CTTCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGTGTGACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GNCAGGCCCG GGTCACTCTG 480
139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGTG GCGATCCATC 540
159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCACTNTGC TCCTCCCCCA TGAGGCCTGG 600
179 Q A V P D L N I T A C I X L L P H E A W 198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGTGCGATC 660
199 H F A R I V E L N I L G F L L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGANGAGGT CAGCAGGACA 720
219 V F F N G H I L A S L R T R E E V 238

721 AGAGTGCGNGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCAAGCT CGTGGTTGTC 780
239 R V X G P K D S K T T A L I L T L V V A 258

781 TTCTTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCCTTC TGAATTCCT ATTCCAGGTG 840
259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
279 Q A V R G C F W E D F I D L G L Q L A N 298

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Figure 21B

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901 TTCTTTGCTT TCACTAACAG CTCCTGAAT CCAGTAATTT ATGCTTTGT GGGCCNGCTC 960
299 F F A F T N S S L N P V I Y V F V G X L 318

961 TTCAGSACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

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Figure 22A

1 AATTCAGAGC CACCGCGGCG AGCGGGGCGAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60
 61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCCA TAAAAGCCT TCCACCCTCC TGTCTGCTTT 120
 121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTGTGTGA 180
 181 CAGATAGTAG GCTTTACGCC TAGCTTGAAG ATGGATAAGC TCCTCCCGTT GGACTCAGAC 240
 1 M D N V L P V D S D 10
 241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCAATC AGTTCGTGCA ACCAGCCTGG 300
 11 L S P N I S T N T S E P N Q F V Q P A W 30
 301 CAAATTGTCC TTTGGGCGAG TGCCTACAGG GTCATTTGTG TGACCTCTGT GGTGGGCAAC 360
 31 Q I V L W A A A Y T V I V V T S V V G N 50
 361 GTGGTAGTGA TGTGGATCAT CTAGCCCAAC AAAAGAATGA GGACAGTGAC GAACTATTTT 420
 51 V V V M W I I L A H K R M R T V T N Y F 70
 421 CTGGTGAACC TGGCCTTCGC GGAGGCCCTCC ATGGCTGCAT TCAATACAGT GGTGAACCTG 480
 71 L V N L A F A E A S M A A F N T V V N F 90
 481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACAACCTC 540
 91 T Y A V H N E W Y Y G L F Y C K F H N F 110
 541 TTNCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600
 111 F P I A A V F A S I Y S M T A V A F D R 130
 601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTGAG CCACAGCCAC CAAAGTGGTC 660
 131 Y M A I I H P L Q P R L S A T A T K V V 150
 661 ATCTGTGTCA TTTGGGTCCT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTACTCAACC 720
 151 I C V I W V L A L L L A F P Q G Y Y S T 170
 721 ACAGAGACCA TGCCCGAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780
 171 T E T M P S R V V C M I E W P E H P N K 190
 781 ATTTATGAGA AAGGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCTGCTG 840
 191 I Y E K V Y H I C V T V L I Y F L P L L 210
 841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGCCAGTAGT GATCCCCGGG 900
 211 V I G Y A Y T V V G I T L W A S E I P G 230
 901 GACTCTCTCT ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAATATGAT 960
 231 D S S D R Y H E Q V S A K R K V V K M M 250

Figure 22B

961 ATTGTCGTGG TGTGCACCTT GCACATCTGC TGGCTGCCCT TCCACATCTT CTTCCTCCTG 1020
 251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA COTGGCCATC 1080
 271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140
 291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCCTGC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200
 311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
 331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320
 351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCNTCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
 371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440
 391 D S K T M T E S F S F S S N V L S * 407

1441 GGGCCTTTGG CAGGTGCAGC CCCCACTGCC TTTGACCTGC CTCCCCTTCAT GCATGGAAT 1500

1501 TCCCTTCATC TGGAAACATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGTCAGTA 1560

1561 TGGGTTTAGG AAAACATTC ATCCTTGAGT CAAAAAATCT CAATCTTCC CTATCTTTGC 1620

1621 CACCCTCATG CTGTGTGACT CAAACCAAAAT CACTGAACCT TGCTAGGCT GTAAAATAAA 1680

1681 AGGTCGGACC AGCTTTTCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATCGAG TGCTCATTTC AGGATG 1766

Figure 23A

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1  AGTCTGCACT  GGAGCTGCCT  GGTGACCAGA  AGTTTGGAGT  CCGCTGACGT  CGCCGCCACG  60

61  ATGGCCTCCA  GGCTGACCCT  GCTGACCCTC  CTGTGCTGTC  TGCTGGCTGG  GGATAGAGCC  120
1  M  A  S  R    L  T  L    L  T  L    L  L  L  L    L  A  G    D  R  A    20

121 TCCTCAAATC  CAAATGCTAC  CAGTCCAGC  TCCAGGATC  CAGAGAGTT  GCAAGACAGA  180
21 S  S  N  P    N  A  T    S  S  S    S  Q  D  P    E  S  L    Q  D  R    40

181 GCGCAAGGGA  AGGTCGCAAC  AACAGTTATC  TCCAAGATGC  TATTCGNTGA  ACCCATCTCG  240
41 G  E  G  K    V  A  T    T  V  I    S  K  M  L    F  X  E    P  I  L    60

241 GAGGTTTCCA  GCTTGCCGAC  AACCAACTCA  ACAACCAATT  CAGCCACCAA  AATAACAGCT  300
61 E  V  S  S    L  P  T    T  N  S    T  T  N  S    A  T  K    I  T  A    80

301 AATACCACCTG  ATGAACCCAC  CACACAACCC  ACCACAGAGC  CCACCACCCA  ACCCACCATC  360
81 N  T  T  D    E  P  T    T  Q  P    T  T  E  P    T  T  Q    P  T  I    100

361 CAACCCACCC  AACCAACTAC  CCAGCTCCCA  ACAGATTCTC  CTACCCAGCC  CACTACTGGG  420
101 Q  P  T  Q    P  T  T    Q  L  P    T  D  S  P    T  Q  P    T  T  G    120

421 TCCTTCTGCC  CAGGACCTGT  TACTCTCTGC  TCTGACTTGG  AGAGTCATTC  AACAGAGGCC  480
121 S  F  C  P    G  P  V    T  L  C    S  D  L  E    S  H  S    T  E  A    140

481 GTGTTGGGGG  ATGCTTTGGT  AGATTTCCTC  CTGAAGCTCT  ACCACGCCTT  CTCAGNAATG  540
141 V  L  G  D    A  L  V    D  F  S    L  K  L  Y    H  A  F    S  X  M    160

541 AAGAAGGTGG  AGACCAACAT  GGCCTTTTCC  CCATTCAAGA  TCGCCAGCCT  CCTTACCCAG  600
161 K  K  V  E    T  N  M    A  F  S    P  F  S  I    A  S  L    L  T  Q    180

601 GTCTCTCTCG  GGGCTGGGCA  GAACACCAAA  ACAAACTGG  AGAGCATCTC  CTCTTACCCC  660
181 V  L  L  G    A  G  Q    N  T  K    T  N  L  E    S  I  L    S  Y  P    200

661 AAGGACTTCA  CCTGTGTCCA  CCAGGCCCTG  AAGGCTTCA  CGACCAAAGG  TGTACCTCA  720
201 K  D  F  T    C  V  H    Q  A  L    K  G  F  T    T  K  G    V  T  S    220

721 GTCTCTCAGA  TCTTCCACAG  CCCAGACCTG  GCCATAAGGG  ACACCTTTGT  GAATGCCTCT  780
221 V  S  Q  I    F  H  S    P  D  L    A  I  R  D    T  F  V    N  A  S    240

781 CGGACCCCTG  ACAGCAGCAG  CCCCAGAGTC  CTAAGCAACA  ACAGTGACGC  CAACTTGGAG  840
241 R  T  L  Y    S  S  S    P  R  V    L  S  N  N    S  D  A    N  L  E    260

841 CTCATCAACA  CCTGGGTGGC  CAAGAACACC  AACAACAAGA  TCAGCCGGCT  GCTAGACAGT  900
261 L  I  N  T    W  V  A    K  N  T    N  N  K  I    S  R  L    L  D  S    280

901 CTGCCCTCCG  ATACCCGCCT  TGTCTCTCTC  AATGCTATCT  ACCTGAGTGC  CAAGTGGAG  960
281 L  P  S  D    T  R  L    V  L  L    N  A  I  Y    L  S  A    K  W  K    300

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Figure 23B

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961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020
301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCAATTGA CCAAACCTTG 1080
321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140
341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGSCTC TCAGCCCTTC TGTTCCTAAG 1200
361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC 1260
381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACAGNCA GATATGCTC TCAATCATGG AGAAATGGA ATCTCTCGAT 1320
401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGSACC CAGATCTTCA GGTTCCTGCG 1380
421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAAC TGACA GAGACTGGGG TGGAGGCGGC TGCAGCTCC 1440
441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTGAAGTGC AGCAGCCCTT CCTCTCTC 1500
461 A I S V A R T L L V F E V Q Q P F L F X 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCCTCAG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCTGAG GGTCTGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

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Figure 24

1 TCCTCCACCT GCTGGCCCTT GGACACCTCT GTCACCATGT GGTTCCTGTT TCTGTGCTTC 60
 1 M W F L V L C L 8
 61 GCCTGTGTC TGGGGGGGAC TGGTGTGCTG CCCCCTGATC AGTCCCGGAT TGTGGGAGGC 120
 9 A L S L G G T G A A P P I Q S R I V G G 28
 121 TGGGAGTGTG AGCAGCATTC CCAGCCCTGG CAGGCGGCTC TGTACCATTT CAGCACTTTT 180
 29 W E C E Q H S Q P W Q A A L Y H F S T F 48
 181 CAGTGTGGGG GCATCTGCTT GCACCCGAG TGGTGTCTCA CAGCTGTCTA TTGCATCAGC 240
 49 Q C G G I L V H R Q W V L T A A H C I S 68
 241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTGTT AGCAGCAAAA CACAGCCGAG 300
 69 D N Y Q L W L G R H N L F D D E N T A Q 88
 301 TTTGTTCATG TCAGTGAGAG CTTCACACAC CCTGGCTTCA ACATGAGCCT CCGTGGAGAA 360
 89 F V H V S E S F P H P G F N M S L L E N 108
 361 CACACCCGCC AAGCAGACGA GGAATACAGC CAGACCTCA TGCTGTCTCC CCGTGCAGAG 420
 109 H T R Q A D E D Y S H D L M L L R L T E 128
 421 CCTGCTGATA CCATCAGAGA TGCTGTGAAG GTCGTGGAGT TGCCCAACNA GGAACCCGAA 480
 129 P A D T I T D A V K V V E L P T X E P E 148
 481 GTGGGGAGCA CCTGTTTGGC TTCCGGCTGG GGCAGCATCG AACCAGAGAA TTTCATCTTT 540
 149 V G S T C L A S G W G S I E P E N F S F 168
 541 CCAGATGATC TCCAGTGTGT GGACCTCAAA ATCCTGCCTA ATGATGAGTG CNAAAAAGCC 600
 169 P D D L Q C V D L K I L P N D E C X K A 188
 601 CACGTCCAGA AGGTGACAGA CTTCATGCTG TGTGTGCGAC ACCTGGAAGG TGGCAAAGAC 660
 189 H V Q K V T D F M L C V G H L E G G K D 208
 661 ACCTGTGTGG GTGATTCAGG GGGCCCGCTG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720
 209 T C V G D S G G P L M C D G V L Q G V T 228
 721 TCATGGGGCT ACGTCCCTTG TGGCACCCCT AATAAGCCTT CTGTGCGCGT CAGAGTGTCT 780
 229 S W G Y V P C G T P N K P S V A V R A V L 248
 781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAAT CCTGAACGCG CAGCCCTGTC 840
 249 S Y V K W I E D T I A E N S * 262
 841 CCCTACCCCC AGTAAAAATCA AATGTGCATC C 871

Figure 25A

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1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGFGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGTGCGCGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CTTTTTTGTC 180
39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTGTGCTCT TCCTCCTGCC CCGCGGCGAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAATGG GGTATCAAG 360
99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTGTG TCATCAGCAT CTTCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGTGTGACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTACCTGTC 480
139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCGCTGG 600
179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGT CAGCAGGACA 720
219 V F F N Y H I L A S L R T R E E V G CAG 238

721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCAGCTG CGTGGTTGTC 780
239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCTCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAAATTCTT ATTCCAGGTG 840
259 F L V C W A P Y H F F A F L E F L F P Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
279 Q A V R G C F W E D F I D L G L Q L A N 298

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Figure 25B

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901 TTCTTTGCCT TCACTAACAG CTCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCIGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTCTGCGC GGAATTAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

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Figure 26A

1 CTGTGCATGG CATCATCCTG GCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
 1 M A S S W P P L E L Q S S N Q S Q L 18

 61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19 F P Q N A T A C D N A P E A W D L L H R 38

 121 GTGTGCGCGA CATTATCAT CTCCATCTGT TTCTTCGGGC TCCTAGGGAA CTTTTTGTG 180
 39 V L P T F I I S I C F F G L L G N L F V 58

 181 CTGTTGGTCT TCCTCCTGCC CGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59 L L V F L L P R R Q L N V A E I Y L A N 78

 241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
 79 L A A S D L V F V L G L P F W A E N I W 98

 301 AACCAGTTTA ACTGGCCTTT CGGAGCCTC CTCTGCCGTG TCATCAACGG GGTATCAAG 360
 99 N Q F N W P F G A L L C R V I N G V I K 118

 361 GCCAATTGTG TCATCAGCAT CTCTCTGGTG GTGGCCATCA GCCAGGACCG CTACGCCGTG 420
 119 A N L F I S I F L V V A I S Q D R Y R V 138

 421 CTGTGCACCC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GACAGGCCCG GGTCACTGCG 480
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

 481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
 159 V L I W V V G G L L S I P T F L L R S I 178

 541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCCTGG 600
 179 Q A V P D L N I T A C I L L L P H E A W 198

 601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
 199 H F A R I V E L N I L G F L L P L A A I 218

 661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGT CAGCAGGACA 720
 219 V F F N Y H I L A S L R T R E E V 238

 721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCAGCTG CGTGGTTGCG 780
 239 R V R G P K D S K T T A L L T L V V A 258

 781 TTCTCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCCTTC TGGAATTCTT ATTCCAGGTG 840
 259 F L V C W A P Y H F F A F L E F L F Q V 278

 841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
 279 Q A V R G C F W E D F I D L G L Q L A N 298

Figure 26B

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901 TTCTTTGCC TCACTAACAG CTCCTGAAT CCAGTAATT ATGTCTTTGT GGSCGGGCTC 960
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCGGGA ACTTTATAAA CAATGCACC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCC ATAGGAAAGA AATCTTCCAA CTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

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Figure 27A

1 CTGTGCATGG CATCATCCTG GCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
 1 M A S S W P P L E L Q S S N Q S Q L 18

 61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19 F P Q N A T A C D N A P E A W D L L H R 38

 121 GTGCTGCCGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTG 180
 39 V L P T F I I S I C F F G L L G N L F V 58

 181 CTGTTGGTCT TCCTCTGCC CGGCGGCAA CTGAACCTGG CAGAAATCTA CCTGCCAAC 240
 59 L L V F L L P R R Q L N V A E I Y L A N 78

 241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTG 300
 79 L A A S D L V F V L G L P F W A E N I W 98

 301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCCGT TCATCAACGG GGTCATCAAG 360
 99 N Q F N W P F G A L L C R V I N G V I K 118

 361 GCCAATTGTG TCATCAGCAT CTTCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
 119 A N L F I S I F L V V A I S Q D R Y R V 138

 421 CTGTGCACCC CTATGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTCACCTGC 480
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

 481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGTG GCGATCCATC 540
 159 V L I W V V G G L L S I P T F L L R S I 178

 541 CAAGCCGCTCC CAGATCTGAA CATCACCGCC TGCATCGTGC TCCTCCCCCA TGAGCCCTGG 600
 179 Q A V P D L N I T A C I V L L P H E A W 198

 601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
 199 H F A R I V E L N I L G F L L P L A A I 218

 661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
 219 V F F N Y H I L A S L R T R E E V C A G 238

 721 AGAGTCCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCAGCTG CGTGGTGTGC 780
 239 R V R G P K D S K T T A L I L T L V V A 258

 781 TTCTCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCCTTC TGGAAATCTT ATTCCAGTGT 840
 259 F L V C W A P Y H F F A F L E F L F F Q V 278

 841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGCCAAC 900
 279 Q A V R G C F W E D F I D L G L Q L A N 298

Figure 27B

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901 TTCTTTGCTT TCACTAACAG CTCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAGAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTCTCTGGC GGAATTAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

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Figure 28A

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1 CTGTGCATGG CATCATCCTG GCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGTGCGCGA CATTATCAT CTCCATCTGT TTCTTGGGCT TCCTAGGGAA CTTTTTTGTC 180
39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTGTGTCT TCCTCCTGCC CGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTATCAAG 360
99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTGTG TCATCAGCAT CTCTCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGTGTGACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTACCTGTC 480
139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATCTCTGCT GCGATCCATC 540
159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACGCCC TGCATCTGTC TCCTCCCCCA TGAAGCCTGG 600
179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTTGCAA GATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GCCTGCGATC 660
199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCATC CTGGCCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
219 V F F N G H I L A S L R T R L K E V V 238

721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCAOGCT CGTGGTTGTC 780
239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCTGTGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAAATCTT ATTCCAGGTG 840
259 F L V C W A P Y H F F A F L E F L F V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
279 Q A V R G C F W E D F I D L G L Q L A N 298

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Figure 28B

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901 TCTTTGCGCT TCACTAACAG CTCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTC TGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTCTCTGGC GGAATTAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

1081 CC 1082

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Figure 29A

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1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGCTGTGTT GTGAGGAGCTC CGTGCCCAACC 60
1 M F S P W K I S M F L S V C E D S V P T 20

61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCAAC TCTTAACGGG 120
21 T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGCGCTGG GCTGGCTCAA CACCATCCAG 180
41 T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCTTCC TCTGGTGCT GTTCGTGCTG GCCACCTAG AGAACATCTT TGTCTCAGC 240
61 P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
81 V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCTGGC CTGCGGGCTG CCCTTCTGGG CCATCAACAT CTCCAACAAC 360
101 A A D L I L A C G L P F W A I T I S N N 120

361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCATTAT CTCCATGAAC 420
121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGGCGG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCGGGAC CATGAAGGAG 600
181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGSCCAAA CGTCACCGCT TGTGTATCA GCTACCCATC CCTCATCTGG 660
201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAGTGTTC AACAATGCT CTTGAATGTC GTGGGCTTCC TGCTGCCCTT GAGTGTATC 720
221 E V F T N M L L N V V G F L L P L T L F I 240

721 ACCTTCTCCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTCAAG 780
241 T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGGAGAGGAG GSCCAGGTG CTAGTCCTGG TTGTGCTGCT GCTATTATC 840
261 E I Q T E R R A T V L V L V V L L T L G I 280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900
281 I C W L P F Q I S T F L D T L H R L G I 300

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Figure 29B

901 CTCTCCAGCT GCCAGGACGA GGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG 960
 301 L S S C Q D E R I I D V I T Q I A S F M 320

 961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
 321 A Y S N S C L N P L V Y V I V G K R F R 340

 1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC 1080
 341 K K S W E V Y Q G V C Q K G G C R S E P 360

 1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
 361 I Q M E N S M G T L R T S I S V E R Q I 380

 1141 CACAACATGC AGGACTGGGC AGGAGACAGA CAGTGAGCAA ACGCCAGCAG GGTGCTGTG 1200
 381 H K L Q D W A G S R Q * 391

 1201 AATTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GCGCCAGGAA TGCCAAGGAG 1260
 1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAAACACC GGAGACTAAT 1320
 1321 TCCTGCCCCG CCCAATTTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380
 1381 GCCAAGGACT CCAAAATCAC AACAGCATTA CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440
 1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500
 1501 CCTCCCGTGT GTTCTCCGTC CCTGCCCCAG CAAGACAATC TAGATCTCCA GGAGAACTGC 1560
 1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTTCTTTAA 1620
 1621 TCTATTACGC TAGAACTTTG AAGGACAATT TCTTGCAATTA ATAAAGGTTA AGCCCTGAGG 1680
 1681 GGTCCTGAT AACAACTGG AGACCAGGAT TTTATGSGCT CCCTCACTGA TGGACAAGGA 1740
 1741 GGCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800
 1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT TCCTATCTTG AAGGAACCTA 1860
 1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTGG ACGAGACGTT 1920
 1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980
 1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAGT 2040

Figure 29C

2041 CGTGTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100
 2101 GTACATGTGA GGCATCATTG CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160
 2161 ACTGAGGTCT AGAAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220
 2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGSCCTC CCTTCCACCT GTCAATCCCA 2280
 2281 CCACCTGAG GCCCAACCG CCACACACAC AGGAGCATTT GGAGAGAAGT CCATGTCTTC 2340
 2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGCTCTGC CCAGAGGATC 2400
 2401 ACAGTCTGTA GACCCCCAC CACCAAGCCG TACCTGGGAA GGGGAGAGT GCAGGCCTGC 2460
 2461 TCAGGACTG TTCTGTGCTC AGCAACCAAG GGATTGTTC TGTCAATCAA TGGTTTATTG 2520
 2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAGG AATGCAATG GTGTTCAACA 2580
 2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTTATTA GCTGGTTGGA 2640
 2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700
 2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760
 2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGCG TAGAACCTGG 2820
 2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGCG TAGAACCTAG 2880
 2881 AAGGCCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940
 2941 GAGGCCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000
 3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACC TGAAGGCTTA GAACCTGGAA GGGCTAGAAC 3060
 3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGCAGGCT AGAACCTGGC AAGCTAGAAC 3120
 3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAAAT AGAAAATTT ACATGGCAAA 3180
 3181 GAGCCATAA ATCCTGACCA ATCCAACCTT GAATTTTAAA GCAAAAAGCGT GAAAAAAGG 3240

Figure 29D

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3241 ATTCCCTCCT TACCCCCAAC CCACTCTTTT TTCCACACAC CCACTCTCCT CTGCCTCAGT 3300
3301 AAGTATCTGG AGGAAGAAAA CAGTGAAAG AAGAAGTAAA AACCATTAG TATTAGTATT 3360
3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAG AGGCTGTGTT 3420
3421 TTGTCACACA GGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480
3481 GCAGAGCTCT GCCGCAATGG CCAATGTGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540
3541 CTGCGGGAGA AGAGCGGCC TATGCATGGT GTAGATGCCC TGATAAAGAA CATCTGTCTT 3600
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTCACATC CAAACGAGAA 3660
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720
3721 AAAAAAAAAA AAA 3733

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Figure 30A

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1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGCTGTGTC GTGAGGAGTC CGTGCCACAC 60
1 M F S P W K I S M F L S V R E D S V P T 20

61 ACGCCTCTT TCAGCCCGCA CATGCTCAAT GTCACCTTGC AAGGCCCCAC TCTTAACGGG 120
21 T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTTGCC AGAGCAAATG CCCCAGTG GAGTGCGTGG GCTGCTCAA CACCATCCAG 180
41 T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCTAG AGAACATCTT TGTCTCAGC 240
61 P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
81 V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCACAAC 360
101 A A D L I L A C G L P F W A I T I S N N 120

361 TTGACTGGC TCTTTGGGGA GACGCTGTC CGCGTGGTGA ATGCATTAT CTCATGAAC 420
121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGT 480
141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGGCGG GATGCGGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGT 540
161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGGT GTACGCTGCT CCTGAGTCA CCCATGCTGG TGTCCGGAC CATGAAGGAG 600
181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAGTGTTC CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCTT GAGTGTCACT 720
221 E V F T N M L L N V V G F L L P L S V I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCTGGG TTGTGCTGCT GCTATTCACT 840
261 E I Q T E R R A T V L V L V V L L G I 280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGSATA CGCTGCATCG CCTCGGCATC 900
281 I C W L P F Q I S T F L D T L H R L G I 300

```

Figure 30B

901 CTCTCCAGCT GCCAGGACGA GGCATCATC GACGTAATCA CACAGATCGC CTCCTTCATG 960
 301 L S S C Q D E R I I D V I T Q I A S F M 320

 961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
 321 A Y S N S C L N P L V Y V I V G K R F R 340

 1021 AAGAACTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAAACC 1080
 341 K K S W E V Y Q G V C Q K G G C R S E P 360

 1081 ATTCAGATGG AGAATCCAT GGGCACACTG CGSACCTCCA TCTCCGTGGA ACGCCAGATT 1140
 361 I Q M E N S M G T L R T S I S V E R Q I 380

 1141 CACAACTGCG AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGTGCTGTG 1200
 381 H K L Q D W A G S R Q * 391

 1201 AATTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GCGCCAGGAA TGCCAAGGAG 1260
 1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAAACAC GGAGACTAAT 1320
 1321 TCCTGCCCTG CCCAATTTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380
 1381 GCCAAGGACT CCAAAATCAC AACAGCATTA CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440
 1441 GCCTGCTCCT TCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500
 1501 CCTCCCGTGT GTTCTCCGTC CCTGCCCCAG CAAGACAAC TAGAATCCA GGAGAACTGC 1560
 1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTCTTTTAA 1620
 1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCAATTA ATAAAGGTTA AGCCCTGAGG 1680
 1681 GGTCCCTGAT AACAACTTGG AGACCAGGAT TTTATGSGCT CCCTCACTGA TGGACAAGGA 1740
 1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800
 1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACTCA 1860
 1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTG ACGAGACGGT 1920
 1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980
 1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAGT 2040

Figure 30C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100
 2101 GTACATGTGA GGCATCAITTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160
 2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGAGAGCCG TGCGGGTGTG 2220
 2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTTGCTC CCTTCACCT GTCAITCCCA 2280
 2281 CCACCTGAG GCCCCAACCG CCACACACAC AGGAGCATTT GGAGAGAAGG CCATGCTTC 2340
 2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTCTTAA TCGGTCTTGC CCAGAGGATC 2400
 2401 ACAGTGTGTA GACCCCCAC CACCAGCCGG TACCTGGGAA GGGGAGAGT GCAGGCCTGC 2460
 2461 TCAGGGAAGT TTCCTGTCTC AGCAACCAAG GGATTGTTC TGTCACATCA TGGTTTATATG 2520
 2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTACCA 2580
 2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTATTA GCTGGTTGGA 2640
 2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700
 2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760
 2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGA TCTGAAGGC TAGAACCTGG 2820
 2821 AGGGCTGGA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880
 2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940
 2941 GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000
 3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACC TGGAGGCTTA GAACCTGGAA GGCTAGAAC 3060
 3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGCAGGCT AGAACCTGGC AAGCTAGAAC 3120
 3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAATG AGAAAAATTT ACATGGCAA 3180
 3181 GAGCCATAA ATCCTGACCA ATCCAACCTCT GAATTTTAAA GCAAAAGCGT GAAAAAAG 3240

Figure 30D

3241 ATTCCCTCCT TACCCCAAC CCACCTCTTTT TTCCACCAC CCACCTCTCT CTGCCTCAGT 3300

3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAG AAGAAGTAA AACCATTAG TATTAGTATT 3360

3361 AGAATGAAGT CAAACTGTGC CACACATGTT GAATGAAAA AAAAAAAGG AGGCTGTGTT 3420

3421 TTGTCACACA GGGCAGTCAT TCAGCACCG AGCAGCTGAT GGTCTGAGAC TCTCTTAGGA 3480

3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540

3541 CTGCGGGAGA AGAGCGGCC TATGCATGTT GTAGATGCC TGATAAGAA CATCTGTCTT 3600

3601 GTGAAAGACT CAATGAGCTG TTAGTGTGTA AACAGGAAG ATTTACATC CAAACGAGAA 3660

3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAA TGGATGAGT TTTTGAAAA 3720

3721 AAAAAAAAAA AAA 3733

Figure 31A

1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTC GTGAGGACTC CGTGCCCAAC 60
 1 M F S P W K I S M F L S V R E D S V P T 20

61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCCAC TCTTAACGGG 120
 21 T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
 41 T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCTTCC TCTGGTGCT GTTCGTGCTG GCCACCTAG AGAACATCTT TGTCTCAGC 240
 61 P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
 81 V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCACAAC 360
 101 A A D L I L A C G L P F W A I T I S N N 120

361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CCGTGGTGA ATGCCATTAT CTCATGAAC 420
 121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
 141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGGCCG GATCGCGGCG GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
 161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTCCGGAC CATGAAGGAG 600
 181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTATCA GCTACCCATC CCTCATCTGG 660
 201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAGTGTTC AACAATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCTC GAGTGTCAAT 720
 221 E V F T N M L L N V V G F L T G T G T G L F I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAGG 780
 241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCAATC 840
 261 E I Q T E R R A T V L V L V V L T G L F I 280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGAAT CGCTGCATCG CCTCGGCATC 900
 281 I C W L P F Q I S T F L D T L H R L G I 300

Figure 31B

901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG 960
 301 L S S C Q D E R I I D V I T Q I A S F M 320

 961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GGTACGTGA TCGTGGGCAA GCGCTTCGA 1020
 321 A Y S N S C L N P L V Y V I V G K R F R 340

 1021 AAGAACTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG AGGGCTGCGC GTCAGAACCC 1080
 341 K K S W E V Y Q G V C Q K E G C R S E P 360

 1081 ATTGAGATGG AGAATCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
 361 I Q M E N S M G T L R T S I S V E R Q I 380

 1141 CACAACTGCG AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
 381 H K L Q D W A G S R Q * 391

 1201 AATTGTGTGA AGGATTGAGG GACAGTTGCT TTTCAGCATG GCGCCAGGAA TGCCAAGGAG 1260
 1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAACACCC GGAGACTAAT 1320
 1321 TCCTGCCCTG CCCAATTITG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380
 1381 GCCAAGGACT CCAAAATCAC AACAGCATTG CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440
 1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500
 1501 CCTCCCGTGT GTTCTCCGTC CTTGCCCCAG CAAGACAATC TAGATCTCCA GGAGAACTGC 1560
 1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTCTTTTAA 1620
 1621 TCTATTGACG TAGAACTTGG AAGGACAATT TCTTGCAITG ATAAAGGTTA AGCCCTGAGG 1680
 1681 GGTCCCTGAT AACAACTGG AGACCAGGAT TTTATGSCCT CCCTCACTGA TGGACAAGGA 1740
 1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800
 1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACCTA 1860
 1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTGG ACGAGACGGT 1920
 1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980
 1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAGT 2040

Figure 31C

2041 CGTTGTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGOTGCTAC 2100
 2101 GTACATGTGA GGCATCATTG CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160
 2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGAGAGCCG TGGCGGTGTG 2220
 2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280
 2281 CCACCTGAG GCCCAACCG CCACACACAC AGGAGCATTG GGAGAGAAGG CCATGCTTC 2340
 2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTCTAA TCGGTCTTGC CCAGAGGATC 2400
 2401 ACAGTGTGA GACCCCCAC CACCAGCCGG TACCTGGGAA GGGGAGAGT GCAGGCCTGC 2460
 2461 TCAGGACTG TTCTGTCTC AGCAACCAAG GGATTGTTC TGTCAATCA TGGTTTATG 2520
 2521 GAAGGTGCC CAGTATGAGC CTTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTACCA 2580
 2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTTTATTA GCTGGTTGGA 2640
 2641 GAGCTAGAAC CTGGAGAGCT AGAACCCTGA GAACCTAGA CTGGAGGGCT AGAACCCTGA 2700
 2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCCTG GAGGGGCTAG AACCTAGAGA AGCTAAAC 2760
 2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGCC TAGAACCTGG 2820
 2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGCC TAGAACCTAG 2880
 2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCCTG 2940
 2941 GAGGGCTAGA ACCTAGAAGG GCTAGAACCCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000
 3001 AGAAGGGCTA GAACTGGAG AGCCAGAAC TGGAGGGCTA GAACCTGGAA GGCCTAGAAC 3060
 3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGCAGGCT AGAACCTGGC AAGCTAGAAC 3120
 3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAGTG AGAAAAATTT ACATGGCAAA 3180
 3181 GAGCCCATAA ATCTGACCA ATCCAACCTCT GAATTTTAAA GCAAAAGCGT GAAAAAAAAG 3240

3241 ATTCCCTCTCT TACCCCAAC CCACTCTTTT TTCCCACCAC CCACTCTCTCT CTGCTCTAGT 3300
3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAG AAGAAGTAA AACCATTTAG TATTAGTATT 3360
3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAGG AGGCTGTGTT 3420
3421 TTGTCACACA GGGCAGTCAT TCAGCACCG AGCAGCTGAT GGTCTGAGAC TCTCTTAGGA 3480
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540
3541 CTGCGGGAGA AGAGCGGCC TATGCATGGT GTAGATGCC TGATAAAGAA CATCTGTCCT 3600
3601 GTGAAAGACT CAATGAGCTG TTAGTGTGTA AACAGGAAGC ATTTCAATC CAAACGAGAA 3660
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGT TTTTGCAAAA 3720
3721 AAAAAAAAAA AAA 3733

Figure 32A

1	CGCCCAACCCAAGTTCAAAGGCTGATAAGAGAGAAAAATCTCATGAGGAGGTTTTAGTCTA	60
61	GGGAAAGTCATTTCAGTGGATGTGATCTTGCTCACAGGGACGATGTCAAGTCTTCCTG	120
1	M S S S S W	6
121	GCTCCTTCTCAGCCTTGTGTCTGTAACGTGCTCAGTCCACCATTGAGGAACAGGCCAA	180
7	L L L S L V A V T A A Q S T I E E Q A K	26
181	GACATTTTGGACAAGTTTAACCACGAAGCCGAAGACCTGTTCTATCAAAGTTCACTTGC	240
27	T F L D K F N H E A E D L F Y Q S S L A	46
241	TTCTTGAATTATAACACCAATATTACTGAAGAGAATGTCCAAAACATGAATAATGTCTGG	300
47	S W N Y N T N I T E E N V Q N M N N A G	66
301	GGACAAATGGTCTGCCTTTTAAAGGAACAGTCCACACTTGCCCAAATGTATCCACTACA	360
67	D K W S A F L K E Q S T L A Q M Y P L Q	86
361	AGAAATTCAGAATCTCAGTCAAGCTTCAGCTGCAGGCTCTTCAGCAAAATGGGTCTTC	420
87	E I Q N L T V K L Q L Q A L Q Q N G S S	106
421	AGTGCTCTCAGAAGACAAGGCAACCGGTTGAACACAATTCTAAATACAATGAGCACCAT	480
107	V L S E D K S K R L N T I L N T M S T I	126
481	CTACAGTACTGGAAAAGTTTGTAACCCAGATAATCCACAAGAAATGCTTATTACTTGAACC	540
127	Y S T G K V C N P D N P Q E C L L L E P	146
541	AGGTTTGAATGAAATAATGGCAAACAGTTTAGACTACAATGAGAGGCTCTGGGCTTGGGA	600
147	G L N E I M A N S L D Y N E R L W A W E	166
601	AAGCTGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATATGAAGAGTATGTGGTCTT	660
167	S W R S E V G K Q L R P L Y E E Y V V L	186
661	GAAAAATGAGATGGCAAGCAAAATCATTTATGAGGACTATGGGATTATGAGAGAGAGA	720
187	K N E M A R A N H Y E D Y G D Y W R G D	206
721	CTATGAAGTAAATGGGGTAGATGGCTATGACTACAGCCGCGGCCAGTTGATTAAGATGT	780
207	Y E V N G V D G Y D Y S R G Q L I E D V	226
781	GGAACATACCTTTGAAGAGATTAAACCATTATATGAACATCTTCATGCCTATGTGAGGGC	840
227	E H T F E E I K P L Y E H L H A Y V R A	246
841	AAAGTTGATGAATGCCTATCCTTCCTATATCAGTCCAATTGGATGCCTCCCTGCTCATTT	900
247	K L M N A Y P S Y I S P I G C L P A H L	266

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0

Figure 32B

901	GCTTGGTGATATGTGGGGTAGATTTTGGACAAATCTGTACTCTTTGACAGTTCCTTTTGG	960
267	L G D M W G R F W T N L Y S L T V P F G	286
961	ACAGAAACCAACATAGATGTTACTGATGCAATGGTGGACCGAGCCTGGGATGCACAGAG	1020
287	Q K P N I D V T D A M V D Q A W D A Q R	306
1021	AATATTCAAGGAGGCCGAGAAGTTCTTTGTATCTGTTGGTCTTCCTAAATGACTCAAGG	1080
307	I F K E A E K F F V S V G L P N M T Q G	326
1081	ATTCTGGGAAAATTCCTAGCTAACGGACCCAGGAAATGTTTCAGAAAGCAGTCTGCCATCC	1140
327	F W E N S M L T D P G N V Q K A V C H P	346
1141	CACAGCTTGGGACCTGGGGAAGGGCGACTTCAGGATCCTTATGTGCACAAAGGTGACAAT	1200
347	T A W D L G K G D F R I L M C T K V T M	366
1201	GGACGACTTCCTGACAGCTCATCATGAGATGGGGCATATCCAGTATGATATGGCATATGC	1260
367	D D F L T A H H E M G H I Q Y D M A Y A	386
1261	TGCACACCTTTTCTGCTAAGAAATGGAGCTAATGAAGGATTCATGAAGCTGTGGGGA	1320
387	A Q P F L L R N G A N E G F H E A V G G E	406
1321	AATCATGTCACTTTCTGCAGCCACACCTAAGCATTTAAATCCATTGGTCTTCTGTCAAC	1380
407	I M S L S A A T P K H L K S I G L L S P	426
1381	CGATTTTCAAGAAGACAATGAAACAGAAATAAACTTCCTGCTCAAACAAGCACTCACGAT	1440
427	D F Q E D N E T E I N F L L K Q A L T I	446
1441	TGTTGGGACTCTGCCATTTACTTTACATGTTAGAGAAGTGGAGGTGGATGGTCTTTAAAGG	1500
447	V G T L P F T Y M L E K W R W M V F K G	466
1501	GGAAATTCCAAAGACCACTGGATGAAAAAGTGGTGGGAGATGAAGCGAGAGATAGTTGG	1560
467	E I P K D Q W M K K W W E M K R E I V G	486
1561	GGTGGTGGAACTGTGCCCCATGATGAAACATACTGTGACCCCGCATCTCTGTCCATGT	1620
487	V V E P V P H D E T Y C D P A S L F H V	506
1621	TTCTAATGATTACTCATTCATTCGATATTACACAAGGACCCCTTTACCAATTCAGTTTCA	1680
507	S N D Y S F I R Y Y T R T L Y Q F Q F Q	526
1681	AGAAGCACTTTGTCAAGCAGCTAAACATGAAGGCCCTCTGCACAAATGTGACATCTCAA	1740
527	E A L C Q A A K H E G P L H K C D I S N	546

Figure 32C

1741	CTCTACAGAAGCTGGACAGAACTGTTCAATATGCTGAGGCTTGGAAAAATCAGAACCCCTG	1800
547	S T E A G Q K L F N M L R L G K S E P W	566
1801	GACCCCTAGCATTTGAAAAATGTTGTAGGAGCAAAGAACATGAATGTAAGGCCACTGCTCAA	1860
567	T L A L E N V V G A K N M N V R P L L N	586
1861	CTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAGAATCTCTTTGTGGGATG	1920
587	Y F E P L F T W L K D Q N K N S F V G W	606
1921	GAGTACCGACTGGAGTCCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCCTAAAAATC	1980
607	S T D W S P Y A D Q S I K V R I S L K S	626
1981	AGCTCTTGGAGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATC	2040
627	A L G D K A Y E W N D N E M Y L F R S S	646
2041	TGTTGCATATGCTATGAGGCAGTACTTTTAAAGTAAAAAAATCAGATGATCTTTTTTGG	2100
647	V A Y A M R Q Y F L K V K N Q M I L F G	666
2101	GGAGGAGGATGTGCGAGTGGCTAAATTTGAAACCAAGAATCTCCTTTAAATTTCTTTGTGAC	2160
667	E E D V R V A N L K P R I S F N F F V T	686
2161	TGCACCTAAAAATGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAGGCCATCAGGAT	2220
687	A P K N V S D I I P R T E V E K A I R M	706
2221	GTCCCGGAGCCGTATCAATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGG	2280
707	S R S R I N D A F R L N D N S L E F L G	726
2281	GATACAGCCAACACTTGGACCTCCTAACCAAGCCCTGTTCCATATGGCTGATTGTTTT	2340
727	I Q P T L G P P N Q P P V S I W L I V F	746
2341	TGGAGTTGTGTGGGAGTGATAGTGGTTGGCATTGTGCATCCTGATCTTCACTGGGATCAG	2400
747	G V V M G V I V V G I V I L I F T G I R	766
2401	AGATCGGAAGAAGAAAAATAAGCAAGAAGTGGAGAAAAATCCTTATGCCTCCATCGATAT	2460
767	D R K K K N K A R S G E N P Y A S I D I	786
2461	TAGCAAAGGAGAAAAATAATCCAGGATTCCAAAACACTGATGATGTTTACAGACCTCCTTTTA	2520
787	S K G E N N P G F Q N T D D V Q T S F *	806
2521	GA AAAATCTATGTTTTTCTCTCTTGAGGTGATTTTGTGTATGTAATGTTAATTCATGG	2580
2581	TATAGAAAATATAAGATGATAAGATATCATTAATGTCAAAACTATGACTCTGTTTCAGA	2640

Figure 32D

2641 AAAAAAATGTCCAAAGACAACATGGCCAAGGAGAGAGCATCTTCATTGACATTGCTTTTC 2700
 2701 AGTATTTAATTTCTGTCCTCGGATTTGACTTCTGTCTCTGTTCTTAATAAGGATTTTGTAT 2760
 2761 TAGAGTATATTAGGGAAGTGTGATTTGGTCTCACAGGCTGTTTCAGGGATAATCTAAAT 2820
 2821 GTAAATGCTCTGTGAATTTCTGAAGTTGAAAACAAGGATATATCATTTGGAGCAAGTGTG 2880
 2881 GATCTTGTATGGAATATGGATGGATCACTTGTAAGGACAGTGCCTGGGAAC TGGTGTAGC 2940
 2941 TGCAAGGATTGAGAATGGCATGCATTAGCTCACTTTCATTTAATCCATTGTCAAGGATGA 3000
 3001 CATGCTTTCTTCACAGTAAC TCAAGTACTATGGTGATTTGCCTACAGTGATGTTT 3060
 3061 GGAATCGATCATGCTTTCTTCAAGGTGACAGGCTAAAGAGAGAAGAAATCCAGGGAACAG 3120
 3121 GTAGAGGACATTGCTTTTTCACTTCCAAGGTGCTTGATCAACATCTCCCTGACAACACAA 3180
 3181 AACTAGAGCCAGGGCCCTCCGTGAAC TCCAGAGCATGCCTGATAGAACTCATTTCTAC 3240
 3241 TGTTCCTCAACTGTGGAGTGAATGGAAAT TCCAAC TGTATGTTCAACCTCTGAAGTGGGT 3300
 3301 ACCCAGTCTCTAAATCTTTTGTATTTGCTCACAGTGTGAGCAGTGTGAGCACAAAG 3360
 3361 CAGACACTCAATAAATGCTAGATTTACACACTCAAAAAAAAAAAAA 3405

Figure 33A

1 ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTTCATATGGC 60
 1 M H L I D Y L L L L L V G L L A L S H G 20

 61 CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG 120
 21 Q L H V E H D G E S C S N S S H Q Q I L 40

 121 GAGACAGGTGAGGGCTCCCCAGCCCTCAAGATAGCCCTGCCAATGCTGACTTTGCGCTTC 180
 41 E T G E G S P S L K I A P A N A D F A F 60

 181 CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGAAGAACATCTTTTCTCCCCGCTG 240
 61 R F Y Y L I A S E T P G K N I F F S P L 80

 241 AGCATCTCGGCGGCTACGCCATGCTTTCCTGGGGGCTGCTCACACAGCCGACGCCAG 300
 81 S I S A A Y A M L S L G A C S H S R S Q 100

 301 ATCCTTGAGGGCTGGGGCTTCAACCTCACCGAGCTGCTGAGTCCGATGTCCATAGGGGC 360
 101 I L E G L G F N L T E L S E S D V H R G 120

 361 TTCCAGCACTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAACACGCGTGGC 420
 121 F Q H L L H T L N L P G H G L E T R V G 140

 421 AGTGCTCTGTTCCTGAGCCACAACTGAAGTTCTTGCAAAATTCCTGAATGACACCATG 480
 141 S A L F L S H N L K F L A K F L N D T M 160

 481 GCCGCTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG 540
 161 A V Y E A K L F H T N F Y D T V G T I Q 180

 541 CTTATCAACGACCAAGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTGGTCAGTGAG 600
 181 L I N D H V K K E T R G K I V D L V S E 200

 601 CTCAAGAAGGAGCTCTTGATGGTGCTGAATTACATTTACTTCAAGCCCTGTGGGAG 660
 201 L K K D V L M V L V N Y I Y F K A L W E 220

 661 AAACCATTCATTTCTCAAGGACCACTCCCAAAGACTTCTATGTTGATGAGAACAACA 720
 221 K P F I S S R T T P K D F Y V D E N T T 240

 721 GTCCGGGTGCCCATGATGCTGCTGAGGACGAGGAGCATCACTGGTATCTTCATGACAGATAC 780
 241 V R V P M M L Q D Q E H H W Y L H D R Y 260

 781 TTGCCCTGCTCGGTGCTACGGATGGATTACAAGGAGACGCAACCGTGTTCATTCCTC 840
 261 L P C S V L R M D Y K G D A T V F F I L 280

Figure 33B

841 CCTAACCAAGGCCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG 900
 281 P N Q G K M R E I E E V L T P E M L M R 300

901 TGGAACTTCTGTCGGAGAGGAATTTTACAAGAAGCTAGAGTTGCATCTTCCCAAG 960
 301 W N N L L R K R N F Y K K L E L H L P K 320

961 TTCTCCATTCTGGCTCCTATGTATTAGATCAGATTTGCCCGAGGCTGGGCTTACGGAT 1020
 321 F S I S G S Y V L D Q I L P R L G F T D 340

1021 CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAACAGCAAAAATGGAGGCATCC 1080
 341 L F S K W A D L S G I T K Q Q K L E A S 360

1081 AAAAGTTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC 1140
 361 K S F H K A T L D V D E A G T E A A A A 380

1141 ACCACGTTGCGCATCAAATTCCTCTCTGCCAGACCAATCGCCACATCCTGCGATTCAAC 1200
 381 T T F A I K F F S A Q T N R H I L R F N 400

1201 CGGCCCTTCCTGTGGTGATCTTTCCACCAGCACCCAGAGTGTCTCTTTCTGGGCAAG 1260
 401 R P F L V V I F S T S T Q S V L F L G K 420

1261 GTCGTCGACCCCAAGAAACCATAG 1284
 421 V V D P T K P * 428

Figure 34A

1 ATGCATCTTATCGACTACCTGCTCCTCTGCTGGTGGACTACTGCGCCCTTCTCATGGC 60
 1 M H L I D Y L L L L L V G L L A L S H G 20

 61 CAGCTGCAGCTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG 120
 21 Q L H V E H D G E S C S N S S H Q Q I L 40

 121 GAGACAGGTGAGGGCTCCCCAGCCTCAAGATAGCCCTGCCAATGCTGACTTTGCGCTTC 180
 41 E T G E G S P S L K I A P A N A D F A F 60

 181 CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGGAAGAACATCTTTTCTCCCGCTG 240
 61 R F Y Y L I A S E T P G K N I F F S P L 80

 241 AGCATCTCGGCGCCTACGCCATGCTTTCCCTGGGGGCTGCTCACACAGCCGACGCCAG 300
 81 S I S A A Y A M L S L G A C S H S R S Q 100

 301 ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGCTCTGAGTCCGATGTCCATAGGGGC 360
 101 I L E G G L G F N L T E L S E S D V H R G 120

 361 TTCCAGCACTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAACACCGCGTGGC 420
 121 F Q H L L H T L N L P G H G L E T R V G 140

 421 AGTGCTCTGTCTCCTGAGCCACAACCTGAAGTTCTTGCAAAATTCCTGAATGACACCATG 480
 141 S A L F L S H N L K F L A K F L N D T M 160

 481 GCGCTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG 540
 161 A V Y E A K L F H T N F Y D T V G T I Q 180

 541 CTTATCAACGACCACGTCAGAAGGAAACTCGAGGGGAAGATTGTGGATTGGTCAGTGAG 600
 181 L I N D H V K K E T R G K I V D L V S E 200

 601 CTCAGAAGGACGCTCTTGATGGTGCTGGTGAATTACATTTACTTCAAAGCCCTGTGGGAG 660
 201 L K K D V L M V L V N Y I Y F K A L W E 220

 661 AAACCATTCATTTCTCAAGGACCACTCCCAAAGACTTTATGTTGATGAGAACAACA 720
 221 K P F I S S R T T P K D F Y V D E N T T 240

 721 GTCCGGTGCCCATGATGCTGCAGGACCAAGGAGCATCACTGGTATCTTCATGACAGATAC 780
 241 V R V P M M L Q D Q E H H W Y L H D R Y 260

 781 TTGCGCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTTTTCATCTTC 840
 261 L P C S V L R M D Y K G D A T V F F I L 280

[illegible][illegible]

Figure 35A

1 ATGCATCTTATCGACTACCTGCTCCTCTGCTGGTTGGACTACTGGCCCTTTCTCATGGC 60
 1 M H L I D Y L L L L L V G L L A L S H G 20

 61 CAGCTGCACGGTTGAGCATGATGGTGAAGTTGACAGTAACAGCTCCCACCAGCAGATTCTG 120
 21 Q L H V E H D G E S C S N S S H Q Q I L 40

 121 GAGACAGGTGAGGGTCCCCAGCCCTCAAGATAGCCCCGCAATGCTGACTTTGCTCTC 180
 41 E T G E G S P S L K I A P A N A D F A F 60

 181 CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGGAAGAATCTTTTCTCCCGCTG 240
 61 R F Y Y L I A S E T P G K N I F F S P L 80

 241 AGCATCTCGGCGGCTACGCCATGCTTCCCTGGGGGCTGCTCACACAGCCGACGCCAG 300
 81 S I S A A Y A M L S L G A C S H S R S Q 100

 301 ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGCTGAGTCCGATGCCATAGGGGC 360
 101 I L E G L G F N L T E L S E S D V H R G 120

 361 TTCCAGCACTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAACACCGCGTGGC 420
 121 F Q H L L H T L N L P G H G L E T R V G 140

 421 AGTGCTCTGTTCTCTGAGCCACAACCTGAAGTTCTTGCAAAATTCCTGAATGACACCATG 480
 141 S A L F L S H N L K F L A K F L N D T M 160

 481 GCCGCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG 540
 161 A V Y E A K L F H T N F Y D T V G T I Q 180

 541 CTTATCAACGACCGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTGGTCAGCGAG 600
 181 L I N D H V K K E T R G K I V D L V S E 200

 601 CTCAAGAAGGCGTCTTGATGGTGGTGAATTACATTTACTTCAAGCCCTGTGGGAG 660
 201 L K K D V L M V L V N Y I Y F K A L W E 220

 661 AAACCATTCATTTCTCAAGGACCACTCCCAAAGACTTCTATGTTGATGAGAACACAA 720
 221 K P F I S S R T T P K D F Y V D E N T T 240

 721 GTCCGGTGCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTTATGACAGATA 780
 241 V R V P M M L Q D Q E H H W Y L H D R Y 260

 781 TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTCATTCTC 840
 261 L P C S V L R M D Y K G D A T V F F I L 280

Figure 35B

841 CCTAACCAAGGCCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG 900
 281 P N Q G K M R E I E E V L T P E M L M R 300

 901 TGGAAACAACCTGTTGCGGAAGAGGAATTTTACAAGAAGCTAGAGTTGCACTCTTCCCAAG 960
 301 W N N L L R K R N F Y K K L E L H L P K 320

 961 TTCTCCATTCTGCTCCTATGTATTAGATCAGATTTTGCCCAAGGCTGGGCTTCACGGAT 1020
 321 F S I S G S Y V L D Q I L P R L G F T D 340

 1021 CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAACAGCAAAAACCTGGAGGCATCC 1080
 341 L F S K W A D L S G I T K Q Q K L E A S 360

 1081 AAAAGTTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGAGCAGCC 1140
 361 K S F H K A T L D V D E A G T E A A A A 380

 1141 ACCACGTCGCGATCAAATTCCTCTCTGCCAGACCAATCGCCACATCCTCGATTCAAC 1200
 381 T T F A I K F F S A Q T N R H I L R F N 400

 1201 CGGCCCTTCCTTGTGGTGATCTTTTCCACCAGCACCCAGAGTGTCCTCTTCTGGGCAAG 1260
 401 R P F L V V I F S T S T Q S V L F L G K 420

 1261 GTCGTCGACCCCAAGAAACCATAG 1284
 421 V V D P T K P * 428

Figure 36A

1 ATGCATCTTATTGACTACCTGCTCCTCCTGCTGGTGGACTACTGGCCCTTTCTCATGGC 60
 1 M H L I D Y L L L L L V G L L A L S H G 20

61 CAGCTGCACGTTGAGCATGATGGTGAGAGTTGAGTAAACAGCTCCCACCAGCAGATTCTG 120
 21 Q L H V E H D G E S C S N S S H Q Q I L 40

121 GAGACAGGTGAGGGCTCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTTGCTCTC 180
 41 E T G E G S P S L K I A P A N A D F A F 60

181 CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGAAGAACATCTTTTCTCCCCGCTG 240
 61 R F Y Y L I A S E T P G K N I F F S P L 80

241 AGCATCTCGGCGGCTACGCCATGCTTTCCTGGGGGCTGCTCACACAGCCGAGCCAG 300
 81 S I S A A Y A M L S L G A C S H S R S Q 100

301 ATCCTTGAAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCATAGGGGC 360
 101 I L E G L G F N L T E L S E S D V H R G 120

361 TTCCAGCACTCTCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAACACGCGTGGC 420
 121 F Q H L L H T L N L P G H G L E T R V G 140

421 AGTGCTCTGTTCTCTGAGCCACAACTGAAGTTCTTGCAAAATTCCTGAATGACACCATG 480
 141 S A L F L S H N L K F L A K F L N D T M 160

481 GCCGCTATGAGGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG 540
 161 A V Y E A K L F H T N F Y D T V G T I Q 180

541 CTTATCAACGACCAGCTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTGGTCAAGGAG 600
 181 L I N D H V K K E T R G K I V D L V S E 200

601 CTCAAGAAGGACGTCTTGATGGTGTGGTGAATTACATTTACTTCAAGCCCTGTGGGAG 660
 201 L K K D V L M V L V N Y I Y F K A L W E 220

661 AAACCATTTATTTCTCAAGGACCACTCCCAAGACTTNTATGTTGATGAGAACACAACA 720
 221 K P F I S S R T T P K D F Y V D E N T T 240

721 GTCCGGGTGCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTTCATGACAGATAC 780
 241 V R V P M M L Q D Q E H H W Y L H D R Y 260

781 TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTTTTCATTCTC 840
 261 L P C S V L R M D Y K G D A T V F F I L 280

Figure 36B

841	CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG	900
281	P N Q G K M R E I E E V L T P E M L M R	300
901	TGGAACAACCTGTTGCGGAAGAGGAATTTTACAAGAAGCTAGAGTTGCATCTTCCCAAG	960
301	W N N L L R K R N F Y K K L E L H L P K	320
961	TTCTCCATTCTGGCTCCTATGTATTAGATCAGATTTTGCCCAAGGCTGGGCTTCACGGAT	1020
321	F S I S G S Y V L D Q I L P R L G F T D	340
1021	CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACAAACAGCAAAAACCTGGAGGCATCC	1080
341	L F S K W A D L S G I T K Q Q K L E A S	360
1081	AAAAGTTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC	1140
361	K S F H K A T L D V D E A G T E A A A A	380
1141	ACCACGTCGCGATCAAATCTTCTCTGCCACAGACCAATCGCCACATCCTGCGATTCAAC	1200
381	T T F A I K F F S A Q T N R H I L R F N	400
1201	CGGCCCTTCTTGTGGTGATCTTTTCCACCAGCACCCAGAGTGTCTCTTTCTGGGCAAG	1260
401	R P F L V V I F S T S T Q S V L F L G K	420
1261	GTCGTCGACCCACGAAACCATAG	1284
421	V V D P T K P *	428

Figure 37A

1	CGCCCAACCCAAAGTTCAAAGGCTGATAAGAGAGAAAAATCTCATGAGGAGGTTT	60
61	GGGAAAGTCATTCAGTGGATGTGATCTTGGCTCACAGGGGACGATGTCAAGCTCTTCTCTG	120
1	M S S S S W	6
121	GCTCCTTCTCAGCCTTGTGTGCTGTAAGTGTGCTCAGTCCACCATTGAGGAACAGGCCAA	180
7	L L L S L V A V T A A Q S T I E E Q A K	26
181	GACATTTTGGACAAGTTTAAACCAAGCGAAGACCTGTTCTATCAAAGTTCACCTTGC	240
27	T F L D K F N H E A E D L F Y Q S S L A	46
241	TTCTTGGAAATTATAACACCAATATTACTGAAGAGAATGTCCAAAACATGAATAATGCTGG	300
47	S W N Y N T N I T E E N V Q N M N N A G	66
301	GGACAAATGGTCTGCCTTTTAAAGGAACAGTCCACACTTGCCTCAAATGTATCCACTACA	360
67	D K W S A F L K E Q S T L A Q M Y P L Q	86
361	AGAAATTCAGAAATCTCACAGTCAAGCTTCAGCTGCAGGCTCTTCAGCAAAATGGGTCTTC	420
87	E I Q N L T V K L Q L Q A L Q Q N G S S	106
421	AGTGCTCTCAGAAGACAAGAGCAACGGTTGAACACAATTCTAAATACAATGAGCACCAT	480
107	V L S E D K S K R L N T I L N T M S T I	126
481	CTACAGTACTGGA AAAAGTTTGTAACCCAGATAATCCACAAGAATGCTTACTTGAACC	540
127	Y S T G K V C N P D N P Q E C L L L E P	146
541	AGGTTTGAATGAAATAATGGCAACAGTTTAGACTACAATGAGAGGCTCTGGGCTTGGGA	600
147	G L N E I M A N S L D Y N E R L W A W E	166
601	AAGCTGGAGATCTGAGGTGGCAAGCAGCTGAGGCCATTATATGAAGAGTATGTGGTCTTT	660
167	S W R S E V G K Q L R P L Y E E Y V V L	186
661	GAAAAATGAGATGGCAAGAGCAAAATCATTTATGAGGACTATGGGATTATTTGGAGAGGAGA	720
187	K N E M A R A N H Y E D Y G D Y W R G D	206
721	CTATGAAGTAAATGGGGTAGATGGCTATGACTACAGCCGCGGCAGTTGATTGAAGATGT	780
207	Y E V N G V D G Y D Y S R G Q L I E D V	226
781	GGAACATACCTTTGAAGAGATTAAACCATTATATGAACATCTTCATGCCTATGTGAGGGC	840
227	E H T F E E I K P L Y E H L H A Y V R A	246
841	AAAGTTGATGAATGCCTATCCTTCCTATATCAGTCCAATTGGATGCCTCCCTGCTCAATT	900
247	K L M N A Y P S Y I S P I G C L P A H L	266

Figure 37B

901	GCTTGGTGATATGTGGGGTAGATTTTGGACAAATCTGTACTCTTTGACAGTTCCCTTTGG	960
267	L G D M W G R F W T N L Y S L T V P F G	286
961	ACAGAAACCAAACATAGATGTTACTGATGCAATGGTGGACCGGCCTGGGATGCACAGAG	1020
287	Q K P N I D V T D A M V D Q A W D A Q R	306
1021	AATATTCAAGGAGGCCGAGAAGTTCTTTGTATCTGTTGGTCTTCCCTAATATGACTCAAGG	1080
307	I F K E A E K F F V S V G L P N M T Q G	326
1081	ATTCTGGGAAAATTCATGCTAACGGACCCAGGAAATGTTTCAGAAAGCAGTCTGCCATCC	1140
327	F W E N S M L T D P G N V Q K A V C H P	346
1141	CACAGCTTGGGACCTGGGGAAGGGCGACTTCAGGATCCTTATGTGCACAAAGGTGACAA	1200
347	T A W D L G K G D F R I L M C T K V T M	366
1201	GGACGACTTCCTGACAGCTCATCATGAGATGGGGCATATCCAGTATGATATGGCATATGC	1260
367	D D F L T A H H E M G H I Q Y D M A Y A	386
1261	TGCACAACCTTTTCTGCTAAGAAATGGAGCTAATGAAGGATTCATGAAGCTGTTGGGGA	1320
387	A Q P F L L R N G A N E G F H E A V G E	406
1321	AATCATGTCACTTTCTGCAGCCACACCTAAGCATTTAAATCCATTGGTCTTCTGTCAACC	1380
407	I M S L S A A T P K H L K S I G L L S P	426
1381	CGATTTTCAAGAAGACAATGAAACAGAAATAAACTTCTGCTCAAACAAGCACTCACGAT	1440
427	D F Q E D N E T E I N F L L K Q A L T I	446
1441	TGTTGGGACTCTGCCATTTACTTACATGTTAGAGAAGTGGAGGTGGATGGTCTTTAAAGG	1500
447	V G T L P F T Y M L E K W R W M V F K G	466
1501	GGAAATTCCAAAGACCACTGGATGAAAAAGTGGTGGGAGATGAAGCGAGAGATAGTTGG	1560
467	E I P K D Q W M K K W W E M K R E I V G	486
1561	GGTGGTGGAACTGTGCCCATGATGAAACATACTGTGACCCCGCATCTCTGTGTCCATGT	1620
487	V V E P V P H D E T Y C D P A S L F H V	506
1621	TTCTAATGATTACTCATTATTTCGATATTACACAAGGACCCCTTTACCAATTCCAGTTTCA	1680
507	S N D Y S F I R Y Y T R T L Y Q F Q F Q	526
1681	AGAAGCACTTTGTCAAGCAGCTAAACATGAAGGCCCTCTGCACAAATGTGACATCTCAAA	1740
527	E A L C Q A A K H E G P L H K C D I S N	546

Figure 37C

1741	CTCTACAGAAGCTGGACAGAAACTGTTCAATATGCTGAGGCTTGGAAAACTCAGAACCCCTG	1800
547	S T E A G Q K L F N M L R L G K S E P W	566
1801	GACCCTAGCATTTGGAAAAATGTTGTAGGAGCAAAGAACATGAATGTAAGGCCACTGCTCAA	1860
567	T L A L E N V V G A K N M N V R P L L N	586
1861	CTACTTTGAGCCCTTATTTTACCTGGCTGAAAGACCAGAACAGAATTCCTTTGTGGGATG	1920
587	Y F E P L F T W L K D Q N K N S F V G W	606
1921	GAGTACCGACTGGAGTCCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAAATC	1980
607	S T D W S P Y A D Q S I K V R I S L K S	626
1981	AGCTCTTGGAGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATC	2040
627	A L G D K A Y E W N D N E M Y L F R S S	646
2041	TGTTGCATATGCTATGAGGCAGTACTTTTTAAAAGTAAAAATCAGATGATCTTTTTTGG	2100
647	V A Y A M R Q Y F L K V K N Q M I L F G	666
2101	GGAGGAGGATGTGCGAGTGGCTAAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTAC	2160
667	E E D V R V A N L K P R I S F N F F V T	686
2161	TGCACCTAAAAACGTGCTGATATCATTCTCTAGAACTGAAGTGAAGGCCATCAGGAT	2220
687	A P K N V S D I I P R T E V E K A I R M	706
2221	GTCCCGGAGCCGTATCAATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTCTTGGG	2280
707	S R S R I N D A F R L N D N S L E F L G	726
2281	GATACAGCCAACACTTTGGACCTCCTAACCGCCCCCTGTTCCATATGGCTGATTGTTT	2340
727	I Q P T L G P P N Q P P V S I W L I V F	746
2341	TGGAGTTGTGATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAG	2400
747	G V V M G V I V V G I V I L I F T G I R	766
2401	AGATCGGAAGAAGAAAAATAAGCAAGAAGTGGAGAAAAATCCTTATGCCTCCATCGATAT	2460
767	D R K K K N K A R S G E N P Y A S I D I	786
2461	TAGCAAAGGAGAAAAATAATCCAGGATTCCAAACACTGATGATGTTTCAGACCTCCTTTT	2520
787	S K G E N N P G F Q N T D D V Q T S F *	806
2521	GAAAAATCTATGTTTTCCTCTTGAGGTGATTTTGTGTATGTAAATGTTAATTCATGG	2580
2581	TATAGAAATATAAGATGATAAAGATATCATTAATGTCAAACTATGACTCTGTTTCA	2640

Figure 37D

2641 AAAAAAATGTCCAAAGACAACATGGCCAAGGAGAGAGCATCTTCATTGACATTGCTTTC 2700
 2701 AGTATTATTTCTGTCTCTGGATTGACTTCTGTTCTGTTCCTTAATAAGGATTTTGATAT 2760
 2761 TAGAGTATATTAGGGAAGTGTGTATTGGTCTCACAGGCTGTTGAGGATAATCTAAAT 2820
 2821 GTAAATGTCGTGTGAATTTCTGAAGTTGAAAAACAAGGATATATCATTTGGAGCAAGTGTG 2880
 2881 GATCTTGTATGGAATATGGATGGATCACTTGTAAGGACAGTGCCTGGGAAGTGGTGTAGC 2940
 2941 TGCAAGGATTGAGAATGGCATGCATTAGCTCACTTTCATTTAATCCATTGTCAAGGATGA 3000
 3001 CATGCTTTCTTCACAGTAACTCAGTTCAAGTACTATGGTGATTTGCCTACAGTGATGTTT 3060
 3061 GGAATCGATCATGCTTTCTTCAAGGTGACAGGTCTAAAGAGAGAAGAATCCAGGGAACAG 3120
 3121 GTAGAGGACATTGCTTTTTCACCTTCCAAGGTGCTTGATCAACATCTCCCTGACAAACAAA 3180
 3181 AACTAGAGCCAGGGGCCCTCCGTGAAGTCCCAGAGCATGCCTGATAGAACTCATTTCTAC 3240
 3241 TGTTCCTCTAACTGTGGAGTGAATGGAAATCCAACTGTATGTTACCCCTCTGAAGTGGGT 3300
 3301 ACCCAGTCTCTTAAATCTTTGTATTGCTCACAGTGTTTGAGCAGTGTGAGCACAAAG 3360
 3361 CAGACACTCAATAAATGCTAGATTTACACACTCAAAAAAAAAAAAA 3405

Figure 38A

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1  ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTNN GTGAGGNCCTC CGTGCCCAACC 60
1  M F S P W K I S M F L S V X E X S V P T 20

61  ACGGCTCTTT TCAGCGCCGA CATGCTCAAT GTCACCTGTC AAGGGCCCCA TCTTAACGGC 120
21  T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTTGGCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
41  T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCTAG AGAACATCTT TGTCTCAGC 240
61  P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
81  V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCTCTGCC CTGCGGGCTG CCCTTCTGGG CCATCACCAT TCACAACAAC 360
101 A A D L I L A C G L P F W A I T I S N N 120

361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT TCACATGAAC 420
121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGGCGG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCGGGAC CATGAAGGAG 600
181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAGTGTTC AACAATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCTC GAGTGTCACT 720
221 E V F T N M L L N V V G F L L P L T 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAG 780
241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGT CGGAGAGGAG GCCACGGTGT CTAGTCCTGG TTGTGCTGCT GCTATTCACT 840
261 E I Q T E R R A T V L V L V V L L L F I 280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGSATA CGCTGCATCG CCTCGGCATC 900
281 I C W L P F Q I S T F L D T L H R L G I 300

```

Figure 38B

901 CTCTCCAGCT GCCAGGACGA GGCATCATC GANGTAATCA CACAGATCGC CTCCTTCATG 960
 301 L S S C Q D E R I I D V I T Q I A S F M 320

 961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
 321 A Y S N S C L N P L V Y V I V G K R F R 340

 1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG NGGGCTGCAG GTCAGAACCC 1080
 341 K K S W E V Y Q G V C Q K X G C R S E P 360

 1081 ATTCCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
 361 I Q M E N S M G T L R T S I S V E R Q I 380

 1141 CACAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
 381 H K L Q D W A G S R Q * 391

 1201 AATTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260
 1261 ACATCTATGC ACGACCTGG GAAATGAGTT GATGTCTCCG GTAAACACCC GGAGACTAAT 1320
 1321 TCCTGCCCTG CCCAATTITG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380
 1381 GCCAAGGACT CCRAAATCAC AACAGCATT CTGTCTTAT TTGCTGCCAC ACCTGAGCCA 1440
 1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500
 1501 CCTCCCTGTG GTTCTCCGTC COTGCCCCAG CAAGACAAC TAGATCTCCA GGAGAACTGC 1560
 1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTCTTTTAA 1620
 1621 TCTATTACAG TAGAACTTIG AAGGACAATT TCTTGCAATTA ATAAAGGTTA AGCCCTGAGG 1680
 1681 GGTCCCTGAT AACAACTTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740
 1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCGAT 1800
 1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACCTA 1860
 1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTG ACGAGACGTT 1920
 1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980
 1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAGT 2040

Figure 38C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAAGCAA AGGGTGCTAC 2100
 2101 GTACATGTGA GGCAATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160
 2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220
 2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280
 2281 CCACCTGAG GCCCAACCG CCACACACAC AGGAGCATTT GGAGAGAAGG CCATGCTCTC 2340
 2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400
 2401 ACAGTGCTGA GACCCCCAC CACCAGCCGG TACCTGGGAA GGGGGAGAGT GCAGGCCTGC 2460
 2461 TCAGGGACTG TTCTGTCTTC AGCAACCAAG GGAATTGTTC TGTCAATCAA TGGTTTATATG 2520
 2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTACACA 2580
 2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTTTATTA GCTGGTTGGA 2640
 2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700
 2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760
 2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820
 2821 AGGGCTGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880
 2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940
 2941 GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000
 3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACC TGGAGGGCTA GAACCTGGAA GGCCTAGAAC 3060
 3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120
 3121 CTGGAGGGAA TGAACCTGGA GGCCTAGAAC CTGGAGAATG AGAAAAATTT ACATGGCAAA 3180
 3181 GAGCCCATAA ATCTTGACCA ATCCAACCTCT GAATTTTAAA GCAAAGCGT GAAAAAAAAG 3240

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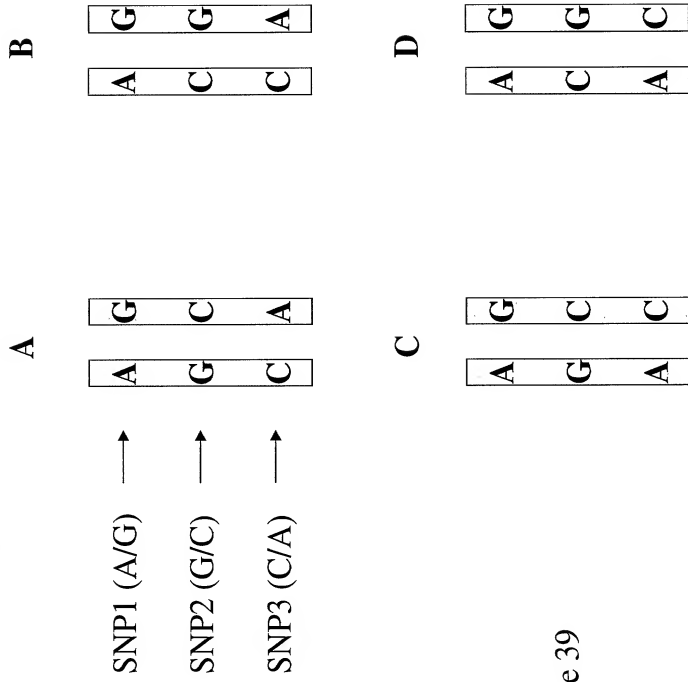


Figure 39

Figure 40

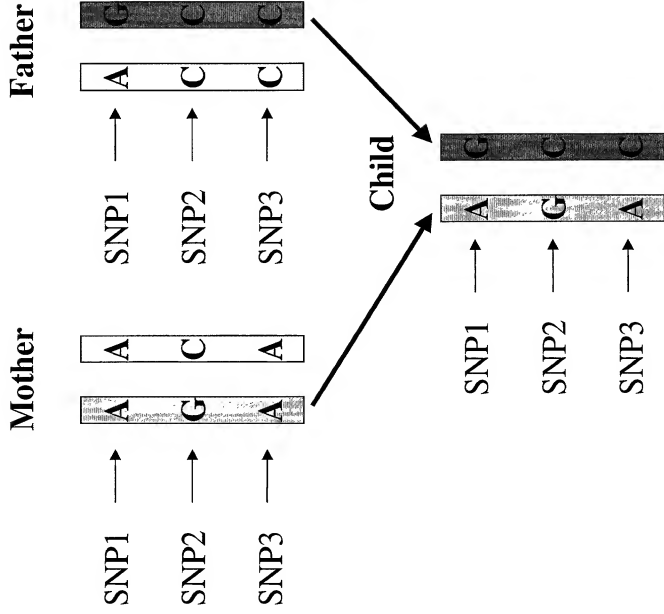


Figure 41A

1 CACCCTATCC TACACTACTA GGAACCTTGCA CAGTCCGCCT CGGCGAGCCC AAAGCTCCTC 60
 61 TGCCCAACCT GGCTCCCAAA ACCCTCCAAA ACAAAGAGCC AGAAAAGCAC TCTCCACCCA 120
 121 GCAGCCAAAC GCCTCCTTCT TGACGCCAGC CCCCAACCTC TGTCTGCTCG AGCCCGAGAA 180
 181 AGGCTGAAG GAACAGGCCG GGAAGGAGC CCTCCCTCTC TCCCTTGTCC CTCATCCAC 240
 241 CCAGCGCCGG CATCTGGAGA CCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300
 1 M A R A H W G C C P W L 12
 301 GTCTCTCTCT GTGCTTGTGC CTGGGGCCAC ACAAAGCCAC TGGACCTTGG AGGCGAGGAT 360
 13 V L L C A C A W G H T X P L D L G G Q D 32
 361 GTGAGAAATT GTTCCACCAA CCCCCCTTAC CTTCAGTTA CTGTGGTCAA TACCACAATG 420
 33 V R N C S T N P P Y L P V T V V N T T M 52
 421 TCACTCAGAG CCTCCGCCA GCAGATGCAG ACCCAGAATC TCTCAGCCTA CATCATCCCA 480
 53 S L T A L R Q Q M Q T Q N L S A Y I I P 72
 481 GGCACAGATG CTCACATGAA CGAGTACATC GGCCAACATG ACGAGAGGCG TGGTGGATT 540
 73 G T D A H M N E Y I G Q H D E R R A W I 92
 541 ACAGGCTTTA CAGGCTCTGC AGGAACTGCA GTGGTGACTA TGAAGAAAGC AGCTGTCTGG 600
 93 T G F T G S A G T A V V T M K K A A V W 112
 601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAATGG ACTGTAATTG GGAGCTCCAT 660
 113 T D S R Y W T Q A E R Q M D C N W E L H 132
 661 AAGGAAGTTG GCACCACTCC TATTGTCACT TGGCTCCTCA CCGAGATTCC TGCTGGAGGG 720
 133 K E V G T T P I V T W L L T E I P A G G 152
 721 CGTGTGGGTT TTGACCCCTT CCTCTTGTC ATTGACACT GGGAGAGTTA TGATCTGGCC 780
 153 R V G F D P F L L S I D T W E S Y D L A 172
 781 CTCCAAGCCT CTAACAGACA GCTGGGTGCC ATCACAACCA ATCTTGTGGA CCTGGTATGG 840
 173 L Q G S N R Q L V S I T T N L V D L V W 192
 841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTTATG CCTGCAGGA GCATTTCACA 900
 193 G S E R P P V P N Q P I Y A L Q E A F T 212
 901 GGGGACACTT GGCAGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAAG 960
 213 G S T W Q E K V S G V R S Q M Q K H Q K 232

Figure 41B

961 GTCCCGACTG CCGTCCTTCT GTCGGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020
 233 V P T A V L L S A L E E T A W L F N L R 252

1021 GCCAGTGACA TCCCTATAA CCCCTCTTTC TATTCTACAC CGCTGCTCAC AGACTCTTCT 1080
 253 A S D I P Y N P F F Y S Y T L L T D S S 272

1081 ATTAGGTGTG TTGCAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAATCC 1140
 273 I R L F A N K S R F S S E T L S Y L N S 292

1141 AGTTGCACAG GCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTCG TGACAGCATC 1200
 293 S C T G P M C V Q I E D Y S Q V R D S I 312

1201 CAGGCTACT CATTTGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260
 313 Q A Y S L G D V R I W I G T S Y T M Y G 332

1261 ATCTATGAAA TGATACCAAG GGAGAACTC GTGACAGACA CCTACTCCCC AGTGATGATG 1320
 333 I Y E M I P R E K L V T D T Y S P V M M 352

1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGC GGAC 1380
 353 T K A V K N S K E Q A L L K A S H V R D 372

1381 GCTGTGGCTG TGATCCGGTA CTGGGTCTGG CTGGAGAAGA ACGTGCCCAA AGGCACAGTG 1440
 373 A V A V I R Y L V W L E K N V P K G T V 392

1441 GATGAGTTTT CGGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAACA GTTCTCTCC 1500
 393 D E F S G A E I V D K F R G E E Q F S S 412

1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTTGAATG CTGCCCTGGC CCACTACAGC 1560
 413 G P S F E T I S A S G L N A A L A H Y S 432

1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620
 433 P T K E L N R K L S S D E M Y L L D S G 452

1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCTCT 1680
 453 G Q Y W D G T T D I T R T V H W G T P S 472

1681 GCCTTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740
 473 A F Q K E A Y T R V L I G N I D L S R L 492

1741 ATCTTTTCCG CTGCTACATC AGGGCGAATG GTGGAGGCCT TTGCCCGCAG AGCCTTGTGG 1800
 493 I F P A A T S G R M V E A F A R R A L W 512

1801 GATGTGTGTC TCAATTATGG TCATGGGACA GGCCACGGCA TTGGCAACTT CCTGTGTGTG 1860
 513 D A G L N Y G H G T G H G I G N F L C V 532

Figure 41C

1861 CATGAGTGGC CAGTGGGATT CCACTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920
 533 H E W P V G F Q S N N I A M A K G M F T 552

1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTGGGA TCCGTCTCGA AGATGTGGCT 1980
 553 S I E P G Y Y K D G E F G I R L E D V A 572

1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATTT 2040
 573 L V V E A K T K Y P G E L P D L V V S F 592

2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCGCCAGCA TCTCCAGTAC 2100
 593 V P Y D R N L I D V S L L S P E H L Q Y 612

2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGGTC CAGAGCTGCA GAGGCGCCAG 2160
 613 L N R Y Y Q T I R E K V G P E L Q R R Q 632

2161 CTACTAGAGG AGTTTCGAGTG GCTTCAACAG CACACAGAGC CCCTGGCCCG CAGGGCCCCA 2220
 633 L L E E F E W L Q Q H T E P L A A R A P 652

2221 GACACCGCCT CCTGGGCGTC TGTGTTAGTG GTCTCCACCC TTGCCATCTC TGGCTGGAGT 2280
 653 D T A S W A S V L V V S T L A I L G W S 672

2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACC CTCCTCTAG ATGGGGGGCT CCCTGTGCTA 2340
 673 V * 673

2341 GCTCCCCCTCA CCCTGCACCTG AACATACCCC AAGAGCCCTT GCTGGCCCAT TGCCTAGAAA 2400

2401 CCTTTGCATT CATCTCTCTT CTCCAAGACC TATGGAGAAG GTCCACGGCC CCAGGAAACA 2460

2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCCCTG 2520

2521 GGCCCCCTAAT CCCAGGCCCC GAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580

2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGTACAGC TGCTCCCTCC CCGCCAAACA 2640

2641 AAGCCCCAAG AAAACAATGC CCCTACCACC CAAGGCTGCC ATGGTCCCGG GAAAACCCAA 2700

2701 CCGTCAACCG CGTGTGTTGGC GTAACCAGAA CTGTTCCCCC CCACCAAGGC TTAATAATCG 2760

2761 CCCCCACTTT TTAACCATCG TCCATTAAAC ACCTGGTGGG CATAGCCAGA GCTGTTGCGA 2820

2821 CCCAGCCAGG GATGAAAAAT CAACCCCGCA CATGGAACCC ATGATTCCCTA AACCCGGGGT 2880

2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTGGC TGTGGAGTAA 2940

Figure 41D

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2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCCTACCA GAGGTTGGAG AACAAACTTG 3000
3001 GGCAGCCGGA ACCCGTCACT ATTTTAGATT CCTGGCATTG GAGGAGCCCT TTGAACTTTC 3060
3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCA CATTCTCTGG ATGCCCTTTC 3120
3121 ACCTTGTGTG GACAGTGTCT GGTTCCTCCA TTTTACAGAC AGGAAAAC TG AGCTTCAGAC 3180
3181 AGGGGGTGGG CTTTGCCTAA GGCACACAAA ATTTGTTGG GAGTTGATGG GCCCAGATGA 3240
3241 GCCAGCATTG CAGCTGTTTC ACCCTTCAGC AACATGCAGA GTCCTGAGC CCACCTCCCA 3300
3301 GCCCTCTCCT CATTCTCTGA ACCCACTGTG GTGAGAAGAA TTGCTCCGG CCAAAATTGGC 3360
3361 CGTTAGCCAC CTGGGTCAC ATCCTGCTAA GACGTTTAAA ACAGCCTAAC AAAGACACTT 3420
3421 GCCTGTGG 3428

```

Figure 42A

1	CTGTGCATGG	CATCATCTCG	GCCCCCTCTA	GAGCTCCAAT	CCTCCAACCA	GAGCCAGCTC	60
1	M A	S S W	P P L	E L Q S	S N Q	S Q L	18
61	TTCCCTCAAA	ATGCTACGGC	CTGTGACAAT	GCTCCAGAAG	CCTGGGACCT	GCTGCACAGA	120
19	F P Q N	A T A	C D N	A P E A	W D L	L H R	38
121	GTGCTGCCGA	CATTATCAT	CTCCATCTGT	TCTTCGGCC	TCCTAGGGA	CCTTTTGTG	180
39	V L P T	F I I	S I C	F F G L	L G N	L F V	58
181	CTGTTGGTCT	TCCTCTGCT	CCGGCGGCAA	CTGAACGTGG	CAGAAATCTA	CCTGGCCAAC	240
59	L L V F	L L P	R R Q	L N V A	E I Y	S A N	78
241	CTGGCAGCCT	CTGATCTGGT	GTTTGTCTTG	GGCTTGCCT	TCTGGGCAGA	GAATATCTGG	300
79	L A A S	D L V	F V L	G L P F	W A E	N I W	98
301	AACCACTTTA	ACTGGCCTTT	CGGAGCCCTC	CTCTGCCGTG	TCATCAACGG	GGTCATCAAG	360
99	N Q F N	L P F	G A L	L C R V	I N G	V I K	118
361	GCCAATTGT	TCATCAGCAT	CTTCTGGTG	GTGGCCATCA	GCCAGGACCG	CTACCGCGTG	420
119	A N L F	I S I	F L V	V A I S	Q D R	Y R V	138
421	CTGGTGACCC	CTATGGCCAG	CGGAAGGCAG	CAGCGCGGGA	GGCAGGCCCC	GGTCACCTGC	480
139	L V H P	M A S	G R Q	Q R R R	Q A R	V T C	158
481	GTGCTCATCT	GGGTTGTGGG	GGGCCTCTTG	AGCATCCCCA	CATTCTCTGT	GCATCCATC	540
159	V L I W	V V G	G L L	S I P T	F L L	R S I	178
541	CAAGCCGTCC	CAGATCTGAA	CATCACCGCC	TGCATCCTGC	TCCTCCCCCA	TGAGGCCTGG	600
179	Q A V P	D L N	I T A	C I L L	L P H	E A W	198
601	CACCTTGCAG	GGATTGTGGA	GTTAAATATT	CTGGGTTTTC	TCCTACCACT	GGCTGCGATC	660
199	H F A R	I V E	L N I	L G F L	L P L	A A I	218
661	GTCTTCTTCA	ACTACCACAT	CCTGGCCTCC	CTGGAACGC	GGGAGGAGGT	CAGCAGGACA	720
219	V F T C	Y H I	L A S	L R T R	E E V	S R T	238
721	AGAGTGCAGG	GGCCGAAGGA	TAGCAAGACC	ACAGCGCTGA	TCCTCACGCT	CGTGGTTGCC	780
239	R V Q G	P K D	S K T	T A L I	L T L	V V A	258
781	TTCTTGCTCT	GCTGGGCCCC	TTACCACTTC	TTTGCCCTTC	TGGAATCTCT	ATTCCAGGTG	840
259	F L V C	W A P	Y H F	F A F L	E F L	F Q V	278
841	CAAGCAGTCC	GAGGCTGCCT	TTGGGAGGAC	TTCATTGACC	TGGCCTGCA	ATTGGCCAAC	900
279	Q A V R	G C F	W E D	F I D L	G L Q	L A N	298

Figure 42B

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901 TTCTTTGCC TACTAACAG CTCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

1081 CC 1082

```


Figure 43A

1 ATGTCTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTC GTGAGGCGCTC CGTGCCCAACC 60
 1 M F S P W K I S M F L S V R E A S V P T 20

 61 ACGGCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCCAC TCTTAACGGC 120
 21 T A S F S A D M L N V T L Q G P T L N G 40

 121 ACCTTTGCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
 41 T F A Q S K C P Q V E W L G W L N T I Q 60

 181 CCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCTAG AGAACATCTT TGTCTCAGC 240
 61 P P F L W V L F V L A T L E N I F V L S 80

 241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
 81 V F C L H K S S C T V A E I Y L G N L A 100

 301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT TCACAACAAC 360
 101 A A D L I L A C G L P F W A I T I S N N 120

 361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT TCCTCATGAAC 420
 121 F D W L F G E T L C R V V N A I I S M N 140

 421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
 141 L Y S S I C F L M L V S I D R Y L A L V 160

 481 AAAACCATGT CCATGGGCGG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
 161 K T M S M G R M R G V R W A K L Y S L V 180

 541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTCCGGAC CATGAAGGAG 600
 181 I W G C T L L L S S P M L V F R T M K E 200

 601 TACAGCGATC AGGGCCACAA CGTCACCGCT TGTGTATCA GCTACCCATC CCTCATCTGG 660
 201 Y S D E G H N V T A C V I S Y P S L I W 220

 661 GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCTT GAGTGTATC 720
 221 E V F T N M L L N V V G F L L P L S V I 240

 721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGTGCA GAAGTTCAAG 780
 241 T F C T M Q I M Q V L R N N E M Q K F K 260

 781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTATC 840
 261 E I Q T E R R A T V L V L V V L L L F I 280

 841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCCTGGATA CGCTGCATCG CCTCGGCATC 900
 281 I C W L P F Q I S T F L D T L H R L G I 300

Figure 43B

901 CTCTCCAGCT⁺ GCCAGGACGA⁺ GCGCATCATC⁺ GATGTAATCA⁺ CACAGATCGC⁺ CTCCTTCATG⁺ 960
 301 L S S C Q D E R I I D V I T Q I A S F M 320

 961 GCCTACAGCA⁺ ACAGCTGCCT⁺ CAACCCACTG⁺ GTGTACGTGA⁺ TCGTGGGCAA⁺ GCGCTTCCGA⁺ 1020
 321 A Y S N S C L N P L V Y V I V G K R F R 340

 1021 AAGAAGTCTT⁺ GGGAGSTGTA⁺ CCAGGGAGTG⁺ TGCCAGAAAG⁺ GGGGCTGCAG⁺ GTCAGAACCC⁺ 1080
 341 K K S W E V Y Q G V C Q K G G C R S E P 360

 1081 ATTCAAGTGG⁺ AGAAGTCCAT⁺ GGGCACACTG⁺ CGGACCTCCA⁺ TCTCCGTGGA⁺ ACGCCAGATT⁺ 1140
 361 I Q M E N S M G T L R T S I S V E R Q I 380

 1141 CACAAACTGC⁺ AGGACTGGGC⁺ AGGGAGCAGA⁺ CAGTGAGCAA⁺ ACGCCAGCAG⁺ GGCTGCTGTG⁺ 1200
 381 H K L Q D W A G S R Q * 391

 1201 AATTGTGTGA⁺ AGGATTGAGG⁺ GACAGTTGCT⁺ TTTCAGCATG⁺ GGCCAGGAA⁺ TGCCAAGGAG⁺ 1260
 1261 ACATCTATGC⁺ ACGACCTTGG⁺ GAAATGAGTT⁺ GATGTCTCCG⁺ GTAAACACC⁺ GGAGACTAAT⁺ 1320
 1321 TCCTGCCCTG⁺ CCCAATTTTG⁺ CAGGGAGCAT⁺ GGCTGTGAGG⁺ ATGGGGTGAA⁺ CTCACGCACA⁺ 1380
 1381 GCCAAGGACT⁺ CCAAAATCAC⁺ AACAGCATT⁺ CTGTCTTAT⁺ TTGCTGCCAC⁺ ACCTGAGCCA⁺ 1440
 1441 GCCTGCTCCT⁺ TCCAGGAGT⁺ GGAGGAGGCC⁺ TGGGGGAGG⁺ GAGAGGAGTG⁺ ACTGAGCTTC⁺ 1500
 1501 CCTCCCGTGT⁺ GTTCTCCGTC⁺ CCTGCCCCAG⁺ CAAGACAAC⁺ TAGATCTCCA⁺ GGAGAACTGC⁺ 1560
 1561 CATCCAGCTT⁺ TGGTGCAATG⁺ GCTGAGTGCA⁺ CAAGTGAGTT⁺ GTTGCCCTGG⁺ GTTCTTTTAA⁺ 1620
 1621 TCTATTACAG⁺ TAGAACTTTG⁺ AAGGACAATT⁺ TCTTGCATTA⁺ ATAAAGGTTA⁺ AGCCCTGAGG⁺ 1680
 1681 GGTCCCTGAT⁺ AACAACCTGG⁺ AGACCAGGAT⁺ TTTATGGCTC⁺ CCTCACTGA⁺ TGGACAAGGA⁺ 1740
 1741 GGTCTGTGCC⁺ AAAGAAGAAT⁺ CCAATAAGCA⁺ CATATTGAGC⁺ ACTTGCTGTA⁺ TATGAGTAT⁺ 1800
 1801 TGAGCACTGT⁺ AGGCAAGACC⁺ CAAGAAAGAG⁺ AAGGAGCCAT⁺ CTCCATCTTG⁺ AAGGAACCTA⁺ 1860
 1861 AAGACTCAAG⁺ TGGGAACGAC⁺ TGGGCACTGC⁺ CACCACCAGA⁺ AAGCTGTTCG⁺ ACGAGACGGT⁺ 1920
 1921 CGAGCAGGGT⁺ GCTGTGGGTG⁺ ATATGGACAG⁺ CAGAAGGGGG⁺ AGACCAAGGT⁺ TCCAGCTCAA⁺ 1980
 1981 CCAATAACTA⁺ TTGCACAACC⁺ ACCTGTCCTT⁺ GCCTCAGTTC⁺ CCTTTTATGT⁺ AACATGAAGT⁺ 2040

Figure 43C

2041 CGTGTGTAGG GTTAAAGGCA GTAAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100
 2101 GTACATGTGA GGCAATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160
 2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220
 2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCAATTCCA 2280
 2281 CCACCCTGAG GCCCCAAACG CCACACACAC AGGAGCATTT GGAGAGAAGG CCATGTCTTC 2340
 2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400
 2401 ACAGTGCTGA GACCCCCAC CACCAGCCGG TACCTGGGAA GGGGGAGAGT GCAGGCCTGC 2460
 2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTC TGTCAAATCA TGGTTTATATG 2520
 2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAGG AATGGCAATG GTGTTCACCA 2580
 2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTTATTA GCTGGTTGGA 2640
 2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700
 2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAC 2760
 2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGCG TAGAACCTGG 2820
 2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGCG TAGAACCTAG 2880
 2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940
 2941 GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000
 3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACC TGGAGGGCTA GAACCTGGAA GGCTAGAAC 3060
 3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGCAGGCT AGAACCTGGC AAGCTAGAAC 3120
 3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAGTG AGAAAAATTT ACATGGCAAA 3180
 3181 GAGCCATAA ATCTTGACCA ATCCAACTCT GAATTTTAA GCAAAAGCGT GAAAAAAAG 3240

$\frac{1}{2} \frac{d}{dt} \ln \frac{1}{\rho}$	$\frac{1}{2} \frac{d}{dt} \ln \frac{1}{\rho}$	$\frac{1}{2} \frac{d}{dt} \ln \frac{1}{\rho}$	$\frac{1}{2} \frac{d}{dt} \ln \frac{1}{\rho}$	$\frac{1}{2} \frac{d}{dt} \ln \frac{1}{\rho}$
0.00	0.00	0.00	0.00	0.00
0.01	0.01	0.01	0.01	0.01
0.02	0.02	0.02	0.02	0.02
0.03	0.03	0.03	0.03	0.03
0.04	0.04	0.04	0.04	0.04
0.05	0.05	0.05	0.05	0.05
0.06	0.06	0.06	0.06	0.06
0.07	0.07	0.07	0.07	0.07
0.08	0.08	0.08	0.08	0.08
0.09	0.09	0.09	0.09	0.09
0.10	0.10	0.10	0.10	0.10
0.11	0.11	0.11	0.11	0.11
0.12	0.12	0.12	0.12	0.12
0.13	0.13	0.13	0.13	0.13
0.14	0.14	0.14	0.14	0.14
0.15	0.15	0.15	0.15	0.15
0.16	0.16	0.16	0.16	0.16
0.17	0.17	0.17	0.17	0.17
0.18	0.18	0.18	0.18	0.18
0.19	0.19	0.19	0.19	0.19
0.20	0.20	0.20	0.20	0.20
0.21	0.21	0.21	0.21	0.21
0.22	0.22	0.22	0.22	0.22
0.23	0.23	0.23	0.23	0.23
0.24	0.24	0.24	0.24	0.24
0.25	0.25	0.25	0.25	0.25
0.26	0.26	0.26	0.26	0.26
0.27	0.27	0.27	0.27	0.27
0.28	0.28	0.28	0.28	0.28
0.29	0.29	0.29	0.29	0.29
0.30	0.30	0.30	0.30	0.30
0.31	0.31	0.31	0.31	0.31
0.32	0.32	0.32	0.32	0.32
0.33	0.33	0.33	0.33	0.33
0.34	0.34	0.34	0.34	0.34
0.35	0.35	0.35	0.35	0.35
0.36	0.36	0.36	0.36	0.36
0.37	0.37	0.37	0.37	0.37
0.38	0.38	0.38	0.38	0.38
0.39	0.39	0.39	0.39	0.39
0.40	0.40	0.40	0.40	0.40
0.41	0.41	0.41	0.41	0.41
0.42	0.42	0.42	0.42	0.42
0.43	0.43	0.43	0.43	0.43
0.44	0.44	0.44	0.44	0.44
0.45	0.45	0.45	0.45	0.45
0.46	0.46	0.46	0.46	0.46
0.47	0.47	0.47	0.47	0.47
0.48	0.48	0.48	0.48	0.48
0.49	0.49	0.49	0.49	0.49
0.50	0.50	0.50	0.50	0.50
0.51	0.51	0.51	0.51	0.51
0.52	0.52	0.52	0.52	0.52
0.53	0.53	0.53	0.53	0.53
0.54	0.54	0.54	0.54	0.54
0.55	0.55	0.55	0.55	0.55
0.56	0.56	0.56	0.56	0.56
0.57	0.57	0.57	0.57	0.57
0.58	0.58	0.58	0.58	0.58
0.59	0.59	0.59	0.59	0.59
0.60	0.60	0.60	0.60	0.60
0.61	0.61	0.61	0.61	0.61
0.62	0.62	0.62	0.62	0.62
0.63	0.63	0.63	0.63	0.63
0.64	0.64	0.64	0.64	0.64
0.65	0.65	0.65	0.65	0.65
0.66	0.66	0.66	0.66	0.66
0.67	0.67	0.67	0.67	0.67
0.68	0.68	0.68	0.	

3241 ATTCCCTCCT TACCCECAAC CCACTCTTTT TTCCACCAC CCACCTCTCT CTGCCTCAGT 3300

3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAA AACCATTTAG TATTAGTATT 3360

3361 AGAATGAAGT CAAACTGTGC CACACATGTT GAATGAAAA AAAAAAAGG AGGCTGTGTT 3420

3421 TTGTCACACA GGGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480

3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540

3541 CTGCGGGAGA AGAGCGGGCC TATGCATGTT GTAGATGCC TGATAAAGAA CATCTGTCCT 3600

3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTTCAATC CAAACGAGAA 3660

3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720

3721 AAAAAAAAAA AAA 3733

Figure 44A

1 ATGCATCTTATCGACTACCTGCTCCTCTGCTGGTTGGACTACTGGCCCTTCTCATGGC 60
 1 M H L I D Y L L L L L V G L L A L S H G 20

 61 CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG 120
 21 Q L H V E H D G E S C S N S S H Q Q I L 40

 121 GAGACAGGTGAGGGCTCCCCAGCCTCAAGATAGCCCTGCGAATGCTGACTTTGCGCTTC 180
 41 E T G E G S P S L K I A P A N A D F A F 60

 181 CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGAAGAACATCTTTTCTCCCCGCTG 240
 61 R F Y Y L I A S E T P G K N I F F S P L 80

 241 AGCATCTCGGCGGCCTACGCCATGCTTTCCCTGGGGCGCTGCTACACAGCCGACGCCAG 300
 81 S I S A A Y A M L S L G A C S H S R S Q 100

 301 ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGCTCTGAGTCCGATGTCATAGGGGC 360
 101 I L E G L G F N L T E L S E S D V H R G 120

 361 TTCCAGCACTCTGCACTCTCAACCTCCCGGCCATGGGCTGGAACACGCGTGGGC 420
 121 F Q H L L H T L N L P G H G L E T R V G 140

 421 AGTGCTCTGTCTCTGAGCCACAACCTGAAGTTCCTTGCAAAATTCCTGAATGACACCATG 480
 141 S A L F L S H N L K F L A K F L N D T M 160

 481 GCCGCTATGAGGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG 540
 161 A V Y E A K L F H T N F Y D T V G T I Q 180

 541 CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTGGTCAGTGAG 600
 181 L I N D H V K K E T R G K I V D L V S E 200

 601 CTCAAGAAGGACGCTCTTGATGGTGTGGAATTACATTTACTTCAAGCCCTGTGGGAG 660
 201 L K K D V L M V L V N Y I Y F K A L W E 220

 661 AAACCATTCTTTCTCAAGGACCACTCCCAAAGACTTCTATGTTGATGAGAACAACA 720
 221 K P F I S S R T T P K D F Y V D E N T T 240

 721 GTCGGGTGCCCCATGATGCTGCAGGACGAGGAGCATCACTGGTATCTTCATGACAGATA 780
 241 V R V P M M L Q D Q E H H W Y L H D R Y 260

 781 TTGCCCTGCTCGGTGCTACGGATGGATTACAAGGAGACGCAACCGTGTTTTCATTCTC 840
 261 L P C S V L R M D Y K G D A T V F F I L 280

Figure 44B

841	CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG	900
281	P N Q G K M R E I E E V L T P E M L M R	300
901	TGGAACAACCTGTTGCGGAAGAGGAATTTTACAAGAAGCTAGAGTTGCATCTTCCCAAG	960
301	W N N L L R K R N F Y K K L E L H L P K	320
961	TTCTCCATTCTGGCTCCTATGTATTAGATCAGATTTTGCCCAGGCTGGGCTTACGGAT	1020
321	F S I S G S Y V L D Q I L P R L G F T D	340
1021	CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAACAGCAAAAACGGAGGCATCC	1080
341	L F S K W A D L S G I T K Q Q K L E A S	360
1081	AAAAGTTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCCGAGGCTGCAGCAGCC	1140
361	K S F H K A T L D V D E A G T E A A A A	380
1141	ACGACGTTGCGGATCAAATCTTCTCTGCCCAGACCAATCGCCACATCCTGCGATTCAAC	1200
381	T T F A I K F F S A Q T N R H I L R F N	400
1201	CGGCCCTTCCTTGTGGTGATCTTTCCACCAGCACCCAGAGTGTCTCTTTCTGGGCAAG	1260
401	R P F L V V I F S T S T Q S V L F L G K	420
1261	GTCGTCGACCCACGAAACCATAG	1284
421	V V D P T K P *	428

Figure 45A

1 ATGCATCTTATCGACTACCTGCTCCTCTGCTGGTTGGACTACTGGCCCTTTCTCATGGC 60
 1 M H L I D Y L L L L L V G L L A L S H G 20

 61 CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCACACAGCAGATTTCTG 120
 21 Q L H V E H D G E S C S N S S H Q Q I L 40

 121 GAGACAGGTGAGGGCTCCCCAGCCTCAAGATAGCCCTGCCAATGCTGACTTTGCTCTTC 180
 41 E T G E G S P S L K I A P A N A D F A F 60

 181 CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGAAGAACAATCTTTTCTCCCCGCTG 240
 61 R F Y Y L I A S E T P G K N I F F S P L 80

 241 AGCATCTCGGCGCCCTACGCCATGCTTTCCCTGGGGCCTGCTCACACAGCCGAGCCAG 300
 81 S I S A A Y A M L S L G A C S H S R S Q 100

 301 ATCCTTGAGGGCTCGGGCTTCAACCTCACCGAGCTGCTCTGAGTCCGATGTCATAGGGGC 360
 101 I L E G L G F N L T E L S E S D V H R G 120

 361 TTCCAGCACTCTCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAACATTCGCTGGGC 420
 121 F Q H L L H T L N L P G H G L E T C V G 140

 421 AGTGCTCTGTTCTCTGAGCCACAACCTGAAGTTCTTGCAAAATTCCTGAATGACACCATG 480
 141 S A L F L S H N L K F L A K F L N D T M 160

 481 GCCGCTATGAGGCTAAACTCTTCCACACCAACTCTACGACACTGTGGGCACAATCCAG 540
 161 A V Y E A K L F H T N F Y D T V G T I Q 180

 541 CTTATCAACGACCAGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTGGTCAGTGAG 600
 181 L I N D H V K K E T R G K I V D L V S E 200

 601 CTCAAGAAGGACGCTCTGATGGTGCTGGTGAATTACATTTACTTCAAGGCCCTGTGGGAG 660
 201 L K K D V L M V L V N Y I Y F K A L W E 220

 661 AAACCATTCATTTCTCTCAAGGACCACTCCCAAGACTTCTATGTTGATGAGAACAACA 720
 221 K P F I S S R T T P K D F Y V D E N T T 240

 721 GTCGGGTGCCCATGATGCTGCAGGACAGGAGCATCACTGGTATCTTCATGACAGATAC 780
 241 V R V P M M L Q D Q E H H W Y L H D R Y 260

 781 TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTTTTCATTCTC 840
 261 L P C S V L R M D Y K G D A T V F F I L 280

Figure 45B

841	CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG	900
281	P N Q G K M R E I E E V L T P E M L M R	300
901	TGGAACAACCTTGTTCGGGAAGAGGAATTTTACAAGAAGCTAGAGTTGCATCTTCCCAAG	960
301	W N N L L R K R N F Y K K L E L H L P K	320
961	TTCTCCATTCTGGCTCCTATGTATTAGATCAGATTTTGCCCGAGCTGGGCTTCACGGAT	1020
321	F S I S G S Y V L D Q I L P R L G F T D	340
1021	CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAACAGCAAAAATGGAGGCATCC	1080
341	L F S K W A D L S G I T K Q Q K L E A S	360
1081	AAAAGTTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC	1140
361	K S F H K A T L D V D E A G T E A A A A	380
1141	ACCACGTTGCGCATCAAATTCTTCTCTGCCCAGACCAATCGCCACATCCTGCGATTCAAC	1200
381	T T F A I K F F S A Q T N R H I L R F N	400
1201	CGGCCCTTCTTGTGGTGATCTTTCCACCAGCACCAGAGTGTCTCTTTCTGGGCAAG	1260
401	R P F L V V I F S T S T Q S V L F L G K	420
1261	GTCGTCGACCCACGAAACCATAG	1284
421	V V D P T K P *	428

Figure 46A

1 CACCCATATCC TACTACTACTA GGAACCTTGCA CAGTCCGCCT CGGCAGCC C AAAGCTCCTC 60
 61 TGCCACCCCT GGCTCCCAAA ACCCTCCAAA ACAAAAGACC AGAAAAGCAC TCTCCACCCA 120
 121 GCAGCCAAAC GCCTCCTTCT TGACGCCAGC CCCACCCCTC TGTCTGCTCG AGCCAGGAA 180
 181 AGGCCTGAAG GAACAGGCCG GGAAGGAGC CCTCCCTCTC TCCCTTGTC CTTCCATCCAC 240
 241 CCAGCGCCCG CATCTGAGAGA CCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300
 1 M A R A H W G C C P W L 12
 301 GTCCCTCCTCT GTGCTTGTC CTGGGGCCAC ACAAAAGCCAC TGGACCTTGG AGGGCAGGAT 360
 13 V L L C A C A W G H T K P L D L G G Q D 32
 361 GTGAGAAATT GTTCCACCAA CCCCCCTTAC CTTCAGTTA CTGGGTCAA TACCACAATG 420
 33 V R N C S T N P P Y L P V T V V N T T M 52
 421 TCACTCACAG CCCTCCGCCA GCAGATGCAG ACCCAGAATC TCTCAGCCTA CATCATCCCA 480
 53 S L T A L R Q Q M Q T Q N L S A Y I I P 72
 481 GGCACAGATG CTCACATGAA CGAGTACATC GGCCAACATG ACGAGAGGCG TGGCTGGATT 540
 73 G T D A H M N E Y I G Q H D E R R A W I 92
 541 ACAGGCTTTA CAGGCTTGC AGGAACTGCA GTGGTGACTA TGAAGAAAAG AGCTGTCTGG 600
 93 T G F T G S A G T A V V T M K K A A V W 112
 601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAATGG ACTGTAATTG GGAGCTCCAT 660
 113 T D S R Y W T Q A E R Q M D C N W E L H 132
 661 AAGGAAGTTG GCACCCTCC TATGTGTCAC TGGCTCCTCA CCGAGATTCC NGCTGGAGGG 720
 133 K E V G T T P I V T W L L T E I P A G G 152
 721 CGTGTGGGTT TTGACCCCTT CCTCTTGTC ATTGACACT GGGAGAGTTA TGATCTGGCC 780
 153 R V G F D P F L L S I D T W E S Y D L A 172
 781 CTCCAAGCT CTAACAGACA GCTGGTGTC ATCACAACA ATCTTGTTGA CCTGTATGG 840
 173 L Q G S N R Q L V S I T T N L V D L V W 192
 841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTTATG CCCTGCAGGA GCATTCACA 900
 193 G S E R P P V P N Q P I Y A L Q E A F T 212
 901 GGGGACACTT GGCAGAGAAA AGTATCTGTC GTCCGAAGCC AGATGCAGAA GCATCAAAA 960
 213 G S T W Q E K V S G V R S Q M Q K H Q K 232

Figure 46B

961 GTCCCGACTG CCGTCCTTCT GTGCGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020
 233 V P T A V L L S A L E E T A W L F N L R 252

1021 GCCAGTGACA TCCCCTATAA CCCCTTCTTC TATTCTACAC CGCTGCTCAC AGACTCTTCT 1080
 253 A S D I P Y N P F F Y S Y T L L T D S S 272

1081 ATTAGGTGTG TTGCAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAACCTC 1140
 273 I R L F A N K S R F S S E T L S Y L N S 292

1141 AGTTGCACAG GCCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTCG TGACAGCATC 1200
 293 S C T G P M C V Q I E D Y S Q V R D S I 312

1201 CAGGCTACT CATTTGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260
 313 Q A Y S L G D V R I W I G T S Y T M Y G 332

1261 ATCTATGAAA TGATACCAAG GGAGAAACTC GTGACAGACA CCTACTCCCC AGTGTATGATG 1320
 333 I Y E M I P R E K L V T D T Y S P V M M 352

1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGCGGGAC 1380
 353 T K A V K N S K E Q A L L K A S H V R D 372

1381 GCTGTGGCTG TGATCCGGTA CTTGGTCTGG CTGAGAAGA ACGTGCCCAA AGGCACAGTG 1440
 373 A V A V I R Y L V W L E K N V P K G T V 392

1441 GATGAGTTTT CGGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAACA GTTCTCTCCTC 1500
 393 D E F S G A E I V D K F R G E E Q F S S 412

1501 GGACCCAGTT TTGAAACCAT CTCGTGCTAGT GGTTTGAATG CTGCCCTGGC CCACCTACAGC 1560
 413 G P S F E T I S A S G L N A A L A H Y S 432

1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620
 433 P T K E L N R K L S S D E M Y L L D S G 452

1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCTCTC 1680
 453 G Q Y W D G T T D I T R T V H W G T P S 472

1681 GCCTTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740
 473 A F Q K E A Y T R V L I G N I D L S R L 492

1741 ATCTTTCCCG CTCTGACATC AGGGCGAATG GTGGAGGCCT TTGCCCAGAG AGCCTTGTGG 1800
 493 I F P A A T S G R M V E A F A R R A L W 512

1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGCGA TTGGCAACTT CCTGTGTGTG 1860
 513 D A G L N Y G H G T G H G I G N F L C V 532

Figure 46C

1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920
 533 H E W P V G F Q S N N I A M A K G M F T 552

1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTGGGA TCCGTCTCGA AGATGTGGCT 1980
 553 S I E P G Y Y K D G E F G I R L E D V A 572

1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATTT 2040
 573 L V V E A K T K Y P G E L P D L V V S F 592

2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCNGAGCA TCTCCAGTAC 2100
 593 V P Y D R N L I D V S L L S P E H L Q Y 612

2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGGTC CAGAGCTGCA GAGGCGCCAG 2160
 613 L N R Y Y Q T I R E K V G P E L Q R R Q 632

2161 CTACTAGAGG AGTTCGAGTG GCTTCAACAG CACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220
 633 L L E E F E W L Q Q H T E P L A A R A P 652

2221 GACACCGCCT CCTGGGCCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCTC TGGCTGGAGT 2280
 653 D T A S W A S V L V V S T L A I L G W S 672

2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACC CTCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340
 673 V * 673

2341 GCTCCCTCA CCCTGCACGT AACATACCCC AAGAGCCCT GCTGGCCCAT TGCCTAGAAA 2400

2401 CTTTGCATT CATCTCTCT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460

2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCCGT 2520

2521 GGCCCTAAT CCCAGSCCCC GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580

2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGTACTAGC TGCTCCCTCC CCGCCAAACA 2640

2641 AAGCCCCAAG AAAACAATGC CCCTACCACC CAAGGTTGCC ATGGTCCCGG GAAAACCCAA 2700

2701 COTGTACCG CGTGTGTTGGC GTAACAGAA CTGTTCCCC CCACCAAGGC TTAATAATCG 2760

2761 CCCCCACTTT TTAACCATCG TCCATTAAAC AACTGGTGGG CATAGCCAGA GCTGTTCTGA 2820

2821 CCCAGCCAGG GATGAAAAAT CAACCCCGGA CATGGAACCC ATGATTCCCTA AACC CGGGGT 2880

2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTTGGC TGTGAGTAA 2940

Figure 46D

2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCCTACCA GAGGTTGGAG AACAAACTTG 3000
 3001 GGCAGCCGGA ACCCGTCACT ATTTTAGATT CCTGSCATTC GAGGAGCCCT TTGAACCTTC 3060
 3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCA CATTCTTGG ATGCCCTTC 3120
 3121 ACCTTGTTGTG GACAGTGTCT GGTTCCTCCA TTTTACAGAC AGGAAAACCTG AGCTTCAGAC 3180
 3181 AGGGGGTGGG CTTTGCCTAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240
 3241 GCCAGCATTC CAGCTGTTC ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCA 3300
 3301 CCCCTCTCCT CATTCCTGA ACCCACTGTG GTGAGAAGAA TTGCTCCGG CCAAAATTGGC 3360
 3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTTAA ACAGCCTAAC AAAGACACTT 3420
 3421 GCCTGTGG 3428

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